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CONTINUATION-IN-PART APPLICATION

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Transmitted herewith for filing is a **Continuation-in-Part** of International Application No. PCT/US99/07333 which claims the benefit of U.S. Application No. 60/080,671, Filed April 3, 1998.

Inventor(s): Thomas Stormann, Lance G. Hammerland, Laura L. Storjohann, James G. Busby, James E. Garrett, Rachel T. Simin

Title: G-PROTEIN FUSION RECEPTORS AND CHIMERIC GABA_B RECEPTORS

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33 Page(s) of Written Description
7 Page(s) Claims
1 Page(s) Abstract
102 Other: Sequence Listing
116 Sheets of Drawings Informal X Formal

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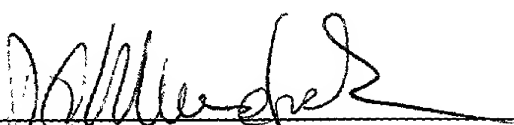
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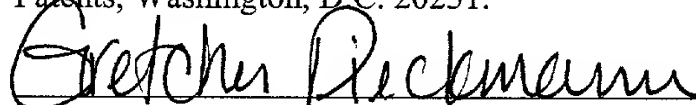
TITLE: G-PROTEIN FUSION RECEPTORS AND
CHIMERIC GABA_B RECEPTORS

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Gretchen Dieckmann

G-PROTEIN FUSION RECEPTORS AND CHIMERIC GABA_B RECEPTORSRELATED APPLICATIONS

5 The present application is a continuation in part of PCT/US99/07333 which claims priority to Garrett *et al.* U.S. Serial No. 60/080,671, filed April 3, 1998, which is hereby incorporated by reference herein in its entirety including the drawings.

FIELD OF THE INVENTION

10 The present invention relates to a G-protein fusion receptors, chimeric GABA_B (γ-aminobutyric acid) receptors, nucleic acid encoding such receptors, and uses of such receptors and nucleic acid encoding such receptors.

BACKGROUND

15 The references cited herein are not admitted to be prior art to the claimed invention.

 Chimeric receptors made up of peptide segments from different receptors have different uses such as being used to assess the functions of different sequence regions and to assess the activity of different compounds at a particular receptor. Examples of using
20 chimeric receptors to assess the activity of different compounds are provided by Dull *et al.*, U.S. Patent No. 4,859,609, Dull *et al.*, U.S. Patent No. 5,030,576, and Fuller *et al.*, U.S. Patent No. 5,981,195.

 Dull *et al.* U.S. Patent No. 4,859,609, and Dull *et al.* U.S. Patent No. 5,030,576, indicate the production and use of chimeric receptors comprising a ligand binding domain
25 of a predetermined receptor and a heterologous reporter polypeptide. The Dull *et al.* patents provide as examples of chimerics: (1) a chimeric receptor made up of the insulin receptor extracellular chain, and the EGF receptor transmembrane and cytoplasmic domains without any HIR B-chain sequence; and (2) a hybrid receptor made up of the v-
erB oncogene product intracellular domain fused to the EGF receptor extracellular and
30 transmembrane domains.

 Fuller *et al.* International Publication No. WO 97/05252 feature chimeric receptors made up of metabotropic glutamate receptor (mGluR) domains and calcium receptor

(CaR) domains. The chimeric receptors allow the coupling of functional aspects of a mGluR with a CaR.

An example of the use of chimeric receptors to assess the functions of different sequence regions receptors are found in studies identifying regions of different guanine nucleotide-binding protein coupled receptors important for guanine nucleotide-binding protein coupling. (See, Kobilka *et al.*, *Science* 240:1310-1316, 1988; Wess *et al.*, *FEBS Lett.* 258:133-136, 1989; Cotecchia *et al.*, *Proc. Natl. Acad. Sci. USA* 87:2896-2900, 1990; Lechleiter *et al.*, *EMBO J.* 9:4381-4390, 1990; Wess *et al.*, *Mol. Pharmacol.* 38:517-523, 1990; and Pin *et al.*, *EMBO J.* 13:342-348, 1994.)

SUMMARY OF THE INVENTION

The present invention features G-protein fusion receptors and chimeric GABA_B receptors (GABA_BRs), nucleic acid encoding such receptors, and the use of such receptors and nucleic acid. G-protein fusion receptors comprise at least one domain from a CaR, a mGluR, and/or a GABA_B receptor fused directly or through a linker to a guanine nucleotide-binding protein (G-protein). Chimeric GABA_BRs comprise at least one of a GABA_BR extracellular domain, a GABA_BR transmembrane domain, or a GABA_BR intracellular domain and one or more domains from a mGluR subtype 8 (mGluR8) and/or a CaR.

G-proteins are peripheral membrane proteins made up of an α subunit, a β subunit, and a γ subunit. G-proteins interconvert between a GDP bound and a GTP bound form. Different types of G-proteins can affect different enzymes, such as adenylate cyclase and phospholipase-C.

Thus, a first aspect of the present invention describes a G-protein fusion receptor comprising:

an extracellular domain comprising an amino acid sequence substantially similar to either an extracellular CaR amino acid sequence, an extracellular mGluR amino acid sequence, or an extracellular GABA_B receptor amino acid sequence;

a transmembrane domain joined to the carboxy terminus of said extracellular domain, said transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to either a transmembrane CaR amino acid sequence, a transmembrane mGluR amino acid sequence, or a transmembrane GABA_B receptor amino acid sequence;

an intracellular domain joined to the carboxy terminus of said transmembrane domain comprising all or a portion of an intracellular amino acid sequence substantially similar to either an intracellular CaR amino acid sequence, an intracellular mGluR amino acid sequence, or an intracellular GABA_B receptor amino acid sequence, provided that
5 said portion is at least about 10 amino acids;

an optionally present linker joined to the carboxy terminus of said intracellular domain, where said optionally present linker is a polypeptide 3 to 30 amino acids in length, wherein said amino acids of the optionally present linker are selected from the group consisting of alanine, proline, serine, and glycine; and

10 a G-protein joined either to said intracellular domain or to said optionally present linker, provided that said G-protein is joined to said optionally present linker when said optionally present linker is present.

“Substantially similar” refers to at least 40% sequence similarity between respective polypeptide regions making up a domain. In preferred embodiments,
15 substantially similar refers to at least 50%, at least 75%, at least 90%, at least 95% sequence similarity, or 100% (the same sequence), between polypeptide domains. The degree to which two polypeptide domains are substantially similar is determined by comparing the amino acid sequences located in corresponding domains. Sequence similarity is preferably determined using BLASTN (Altschul *et al.*, *J. Mol. Biol.* 215:403-
20 410, 1990).

The different receptor components of the G-protein receptor can come from the same receptor protein or from a chimeric receptor made up of different receptor domains. By swapping different domains compounds able to effect different domains of a particular receptor can be identified and the activity of different compounds at different
25 domains can be measured.

In different embodiments the CaR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian CaR, preferably the human CaR; mGluR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian mGluR,
30 preferably a human mGluR; and GABA_BR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian GABA_BR, preferably a human GABA_BR.

In preferred embodiments concerning GABA_BR regions that are present: the GABA_BR extracellular domain is substantially similar to a GABA_BR extracellular domain provided in SEQ. ID. NOs. 2-4; the GABA_BR transmembrane domain is substantially similar to the GABA_BR transmembrane domain provided in SEQ. ID. NOs. 7-9; and the GABA_BR intracellular domain is substantially similar to a GABA_BR intracellular domain provided in SEQ. ID. NOs. 12-14.

In preferred embodiments concerning CaR regions that are present: the CaR extracellular domain is substantially similar to the CaR extracellular provided in SEQ. ID. NO. 1; the CaR transmembrane domain is substantially similar to the CaR transmembrane domain provided in SEQ. ID. NO. 6; and the CaR intracellular domain is substantially similar to the CaR intracellular domain such as that provided in SEQ. ID. NO. 11.

Various different mGluR subtypes present in different organisms, including humans, are described in different patent publications as follows: mGluR₁ - WO 94/29449, EP 569 240 A1, WO 92/10583 and U.S. Patent No. 5,385,831; mGluR₂ - WO 94/29449, WO 96/06167, and EP 711 832 A2; mGluR₃ - WO 94/29449, and WO 95/22609; mGluR₄ - WO 95/08627, WO 95/22609, and WO 96/29404; mGluR₅ - WO 94/29449; mGluR₆ - WO 95/08627; mGluR₇ - U.S. Patent No. 5,831,047, WO 95/08627 and WO 96/29404; and mGluR₈ - U.S. Patent Nos. 6,051,688, 6,077,675, 6,084,084 and EP 816 498 A2. (Each of these references are hereby incorporated by reference herein.)

In preferred embodiments concerning mGluR regions that are present: the mGluR extracellular domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8; the mGluR transmembrane domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8; and the mGluR intracellular domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8. Preferred embodiments also include any mGluR splice variant.

In preferred embodiments concerning the optionally present linker, said optionally present linker is a polypeptide 3 to 30 amino acids in length, wherein said amino acids of the optionally present linker are selected from the group consisting of alanine, proline, serine, and glycine; and more preferably, the optionally present linker is comprised of alanine amino acids.

Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a G-protein fusion receptor, and a cell where the G-protein fusion receptor is expressed. Preferably, the G-protein fusion receptor is functional in the cell.

5 Another aspect of the present invention describes a recombinant cell produced by combining (a) a cell where a G-protein fusion receptor is expressed, and (b) a vector comprising nucleic acid encoding a G-protein fusion receptor and elements for introducing heterologous nucleic acid into the cell. Preferably, the G-protein fusion receptor is functional in the cell.

10 Another aspect of the present invention describes a process for the production of a G-protein fusion receptor. The process is performed by growing host cells comprising a G-protein fusion receptor.

Another aspect of the present invention describes a method of measuring the ability of a compound to affect G-protein fusion receptor activity.

15 Another aspect of the present invention describes a chimeric GABA_BR comprising an extracellular domain, a transmembrane domain and an intracellular domain, wherein at least one domain is from a GABA_BR and at least one domain is from CaR or mGluR8. The extracellular domain comprises an amino acid sequence substantially similar to a CaR extracellular domain (SEQ. ID. NO. 1), a GABA_BR1a extracellular domain (SEQ.
20 ID. NO. 2), a GABA_BR1b extracellular domain (SEQ. ID. NO. 3), a GABA_BR2 extracellular domain (SEQ. ID. NO. 4), or a mGluR8 extracellular domain (SEQ. ID. NO. 5).

The transmembrane domain comprises an amino acid sequence substantially similar to a CaR transmembrane domain (SEQ. ID. NO. 6), a GABA_BR1a transmembrane
25 domain (SEQ. ID. NO. 7), a GABA_BR1b transmembrane domain (SEQ. ID. NO. 8), a GABA_BR2 transmembrane domain (SEQ. ID. NO. 9), or a mGluR8 transmembrane domain (SEQ. ID. NO. 10).

The intracellular domain comprises an amino acid sequence substantially similar to a CaR intracellular domain (SEQ. ID. NO. 11), a GABA_BR1a intracellular domain
30 (SEQ. ID. NO. 12), a GABA_BR1b intracellular domain (SEQ. ID. NO. 13), a GABA_BR2 intracellular domain (SEQ. ID. NO. 14), or a mGluR8 intracellular domain (SEQ. ID. NO. 15).

Preferred chimeric GABA_BRs contain at least one mGluR8 intracellular, transmembrane or extracellular domain, or at least one CaR intracellular, transmembrane or extracellular domain. More preferably, the chimeric GABA_BR contains at least one CaR domain.

5 In preferred embodiments concerning mGluR8 regions that are present: the mGluR8 extracellular domain is substantially similar to the mGluR8 extracellular domain provided in SEQ. ID. NO. 5; the mGluR8 transmembrane domain is substantially similar to the mGluR8 transmembrane domain provided in SEQ. ID. NO. 10; and the mGluR8 intracellular domain is substantially similar to the mGluR8 receptor intracellular provided
10 in SEQ. ID. NO. 15.

Preferably, the domains are functionally coupled such that a signal from the binding of an extracellular ligand is transduced to the intracellular domain when the chimeric receptor is present in a suitable host cell. A suitable host cell contains the elements for functional signal transduction for receptors coupled to a G-protein.

15 Another aspect of the present invention describes a nucleic acid comprising a nucleotide sequence encoding for a chimeric GABA_BR.

Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a chimeric GABA_BR, and a cell where the chimeric GABA_BR is expressed. Preferably, the chimeric GABA_BR is functional in the cell.

20 Another aspect of the present invention describes a recombinant cell produced by combining (a) a cell where a chimeric GABA_BR is expressed, and (b) a vector comprising nucleic acid encoding the chimeric GABA_BR and elements for introducing heterologous nucleic acid into the cell. Preferably, the chimeric GABA_BR is functional in the cell.

Another aspect of the present invention describes a process for the production of a
25 chimeric receptor. The process is performed by growing host cells comprising a chimeric GABA_BR.

Another aspect of the present invention describes a method of measuring the ability of a compound to affect GABA_BR or mGluR activity. The method is performed by measuring the ability of a compound to affect chimeric GABA_BR or mGluR activity.

30 Another aspect of the present invention describes a fusion receptor polypeptide comprising a receptor and a G-protein α subunit, wherein said G-protein α subunit is fused to the intracellular domain of said receptor, provided that the receptor is not an adrenoreceptor.

Various examples are described herein. These examples are not intended in any way to limit the claimed invention.

Other features and advantages of the invention will be apparent from the following drawings, the description of the invention, the examples, and the claims.

5

BRIEF DESCRIPTION OF DRAWINGS

Figures 1a-1d illustrate the amino acid sequences of a human CaR extracellular domain (SEQ. ID. NO. 1), a human GABA_BR1a extracellular domain (SEQ. ID. NO. 2), a human GABA_BR1b extracellular domain (SEQ. ID. NO. 3), a human GABA_BR2
10 extracellular domain (SEQ. ID. NO. 4), and a human mGluR8 extracellular domain (SEQ. ID. NO. 5).

Figures 2a-2b illustrate the amino acid sequences of a human CaR transmembrane domain (SEQ. ID. NO. 6), a human GABA_BR1a transmembrane domain (SEQ. ID. NO. 7), a human GABA_BR1b transmembrane domain (SEQ. ID. NO. 8), a human GABA_BR2
15 transmembrane domain (SEQ. ID. NO. 9), and a human mGluR8 transmembrane domain (SEQ. ID. NO. 10).

Figures 3a-3b illustrate the amino acid sequences of a human CaR intracellular domain (SEQ. ID. NO. 11), a human GABA_BR1a intracellular domain (SEQ. ID. NO. 12), a human GABA_BR1b intracellular domain (SEQ. ID. NO. 13), a human GABA_BR2
20 intracellular domain (SEQ. ID. NO. 14), and a human mGluR8 intracellular domain (SEQ. ID. NO. 15).

Figures 4a-4b illustrate the amino acid sequence of G₁₅ (SEQ. ID. NO. 16) and G₁₆ (SEQ. ID. NO. 17).

Figures 5a-5r illustrate the cDNA sequences encoding for human CaR (SEQ. ID. NO. 18), human GABA_BR1a (SEQ. ID. NO. 19), human GABA_BR1b (SEQ. ID. NO. 20),
25 and human GABA_BR2 (SEQ. ID. NO. 21).

Figures 6a-6h illustrate the cDNA sequence for rat GABA_BR1a (SEQ. ID. NO. 22) and rat GABA_BR1b (SEQ. ID. NO. 23).

Figures 7a-7c illustrate the amino sequence for rat GABA_BR1a (SEQ. ID. NO. 24)
30 and rat GABA_BR1b (SEQ. ID. NO. 25).

Figure 8 illustrates the ability of a chimeric CaR/GABA_BR2 (CaR extracellular and transmembrane domains, and intracellular GABA_BR2 domain) to transduce a signal. Signal production was measured by detecting an increase in the calcium-activated

chloride current. The line in the middle of the increase signifies a wash step.

Figures 9a-9p illustrate the cDNA sequence for human mGluR2 (SEQ. ID. NO. 26), chimeric hCAR/hmGluR2 (SEQ. ID. NO. 30), chimeric hmGluR2/hCaR (SEQ. ID. NO. 34), and chimeric hmGluR8/hCaR (SEQ. ID. NO. 38).

5 Figures 10a-10f illustrate the amino acid sequence for human mGluR2 (SEQ. ID. NO. 27), chimeric hCAR/hmGluR2 (SEQ. ID. NO. 31), chimeric hmGluR2/hCaR (SEQ. ID. NO. 35), chimeric hmGluR8/hCaR (SEQ. ID. NO. 39).

10 Figures 11a-11v illustrate the cDNA sequence for the phCaR/hmGluR2*Gqi5 fusion construct (SEQ. ID. NO. 32), pmGluR2//CaR*G_{qi5} fusion construct (SEQ. ID. NO. 36), pmGluR2//CaR*G_{qi5}+3Ala linker fusion construct (SEQ. ID. NO. 46), and the mGluR8//CaR*G_{qi5} fusion construct (SEQ. ID. NO. 40).

15 Figures 12a-12h illustrate the amino acid sequence for the phCaR/hmGluR2*Gqi5 fusion construct (SEQ. ID. NO. 33), pmGluR2//CaR*G_{qi5} fusion construct (SEQ. ID. NO. 37), pmGluR2//CaR*G_{qi5}+3Ala linker fusion construct (SEQ. ID. NO. 47), and the mGluR8//CaR*G_{qi5} fusion construct (SEQ. ID. NO. 41).

Figures 13a-13m illustrate the cDNA sequence for the GABA-R2*Gqo5 fusion construct (SEQ. ID. NO. 42) and the GABA-BR1a*Gqo5 fusion construct (SEQ. ID. NO. 44).

20 Figures 14a-14e illustrates the amino acid sequence for the GABA-BR2*Gqo5 fusion construct (SEQ. ID. NO. 43) and the GABA-BR1a*Gqo5 fusion construct (SEQ. ID. NO. 45).

25 Figure 15 illustrates the ability of different G-protein fusions to transduce signal resulting from ligand binding. mGluR2//CaR*Gqi5 is shown by SEQ. ID. NO. 37, CaR/mGluR2*Gqi5 is shown by SEQ. ID. NO. 33, mGluR8//CaR*Gqi5 is shown by SEQ. ID. NO. 41.

Figures 16a-16e illustrates the amino acid sequence for the ph8SPmGluR4 chimeric construct (SEQ. ID. NO.48), the amino acid sequence for the phmGluR4//CaR*AAA*Gα_{qi5} fusion construct (SEQ. ID. NO. 49), and the phmGluR8//CaR*AAA*Gα_{qi5} fusion construct (SEQ. ID. NO. 50).

30

DETAILED DESCRIPTION OF THE INVENTION

The CaR, mGluR, and the GABA_BR are structurally similar in that they are each a single subunit membrane protein possessing an extracellular domain, a transmembrane domain comprising seven putative membrane spanning helices connected by three intracellular and three extracellular loops, and an intracellular carboxy-terminal domain.

5 Signal transduction is activated by the extracellular binding of an agonist. The signal is transduced to the intracellular components of the receptor causing an intracellular effect.

Signal transduction from agonist binding to an extracellular region can be modulated by compounds acting at a downstream transmembrane domain or the intracellular domain. Downstream effects include antagonist actions of compounds and
10 allosteric actions of compounds.

The transmembrane domain provides different types of target sites for compounds modulating receptor activity in different environments. As noted above, the transmembrane domain contains extracellular, transmembrane, and intracellular components.

15 Compounds modulating GABA_BR, CaR, or mGluR activity can be obtained, for example, by screening a group or library of compounds to identify those compounds having the desired activity and then synthesizing such compound. Thus, included in the present invention is a method of making a GABA_BR, CaR, or mGluR active compound by first screening for a compound having desired properties and then chemically synthesizing
20 that compound.

Metabotropic Glutamate Receptors (mGluRs)

mGluRs are G protein-coupled receptors capable of activating a variety of intracellular secondary messenger systems following the binding of glutamate (Schoepp *et al.*, *Trends Pharmacol. Sci.* 11:508, 1990; Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993, hereby incorporated by reference herein).

Activation of different mGluR subtypes *in situ* elicits one or more of the following responses: activation of phospholipase C, increases in phosphoinositide (PI) hydrolysis, intracellular calcium release, activation of phospholipase D, activation or inhibition of
30 adenylyl cyclase, increases and decreases in the formation of cyclic adenosine monophosphate (cAMP), activation of guanylyl cyclase, increases in the formation of cyclic guanosine monophosphate (cGMP), activation of phospholipase A₂, increases in arachidonic acid release, and increases or decreases in the activity of voltage- and ligand-

gated ion channels (Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993; Schoepp, *Neurochem. Int.* 24:439, 1994; Pin and Duvoisin, *Neuropharmacology* 34:1, 1995, hereby incorporated by reference herein).

Eight distinct mGluR subtypes have been isolated. (Nakanishi, *Neuron* 13:1031, 1994; Pin and Duvoisin, *Neuropharmacology* 34:1, 1995; Knopfel et al., *J. Med. Chem.* 38:1417; *Eur. J. Neuroscience* 7:622-629, 1995, each of these references is hereby incorporated by reference herein.) The different mGluRs possess a large amino-terminal extracellular domain (ECD) followed by a seven putative transmembrane domain (7TMD) comprising seven putative membrane spanning helices connected by three intracellular and three extracellular loops, and an intracellular carboxy-terminal domain of variable length (cytoplasmic tail).

Human mGluR8 is described by Stormann *et al.*, U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084, and mouse mGluR8 is described by Duvoisin *et al.*, *J. Neurosci.* 15:3075-3083, 1995, (both of these references are hereby incorporated by reference herein). mGluR8 couples to G_i. Agonists of mGluR8 include L-glutamate and L-2-amino-4-phosphonobutyrate.

mGluR8 activity can be measured using standard techniques. For example, G_i negatively couples to adenylate cyclase to inhibit intracellular cAMP accumulation in a pertussis toxin-sensitive fashion. Thus, mGluR8 activity can be measured, for example, by measuring inhibition of forskolin-stimulated cAMP production as described by Duvoisin *et al.*, *J. Neurosci.* 15:3075-3083, 1995.

mGluRs have been implicated in a variety of neurological pathologies. Examples of such pathologies include stroke, head trauma, spinal cord injury, epilepsy, ischemia, hypoglycemia, anoxia, and neurodegenerative diseases such as Alzheimer's disease (Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993; Cunningham *et al.*, *Life Sci.* 54:135, 1994; Pin et al., *Neuropharmacology* 34:1, 1995; Knopfel et al., *J. Med. Chem.* 38:1417, 1995, each of which is hereby incorporated by reference herein).

Calcium Receptor

The CaR responds to changes of extracellular calcium concentration and also responds to other divalent and trivalent cations. The CaR is a G-protein coupled receptor containing an extracellular Ca²⁺ binding domain. Activation of the CaR, descriptions of CaRs isolated from different sources, and examples of CaR active compound are provided

in Nemeth *NIPS* 10:1-5, 1995, Brown *et al.* U.S. Patent No. 5,688,938, Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, Brown E.M. *et al.*, *Nature* 366:575, 1993, Riccardi D., *et al.*, *Proc. Nat'l. Acad. Sci. USA* 92:131-135, 1995, and Garrett J.E., *et al.*, *J. Biol. Chem.* 31:12919-12925, 1995. (Each of these references are hereby incorporated by reference herein.) Brown *et al.* U.S. Patent No. 5,688,938 and Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, describe different types of compounds active at the CaR including compounds which appear to be allosteric modulators and CaR antagonists.

The CaR can be targeted to achieve therapeutic effects. Examples of target diseases are provided in Brown *et al.* U.S. Patent No. 5,688,938, and Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, and include hyperparathyroidism and osteoporosis.

γ -Aminobutyric acid Receptors (GABA_BRs)

GABA_BRs are G-protein coupled metabotropic receptors. GABA_BRs modulate synaptic transmission by inhibiting presynaptic transmitter release and by increasing K⁺ conductance responsible for long-lasting inhibitory postsynaptic potentials. (See, Kaupmann *et al.*, *Nature* 386:239-246, 1997, hereby incorporated by reference herein.)

GABA_BRs are found in the mammalian brain, in locations outside of the brain, and in lower species. Outside of the brain, GABA_BRs have been identified on axon terminals and ganglion cell bodies of the autonomic nervous system, on fallopian tube and uterine intestinal smooth muscle cells, in the kidney cortex, urinary bladder muscle and on testicular interstitial cells. (See, Bowery, *Annu. Rev. Pharmacol. Toxicol.* 33:109-147, 1993, hereby incorporated by reference herein.)

Different GABA_BRs subtypes exist. Kaupmann *et al.*, *Nature* 386:239-246, 1997, indicate that they cloned GABA_BRs. Nucleic acid encoding two GABA_BR proteins were indicated to be cloned from rat brain: GABA_BR1a and GABA_BR1b. GABA_BR1a differs from GABA_BR1b in that the N-terminal 147 residues are replaced by 18 amino acids.

GABA_BR1a and GABA_BR1b appear to be splice variants. The cloned GABA_BRs were indicated to negatively couple adenylyl cyclases and show sequence similarity to the metabotropic receptors for L-glutamate (mGluR). Northern blot analysis indicated that

GABA_BR1a and GABA_BR1b is present in brain and testis, but not in kidney, skeletal muscle, liver, lung, spleen, or heart.

Kaupmann *et al.*, International Application Number PCT/EP97/01370, International Publication Number WO 97/46675, indicate that they have obtained rat
 5 GABA_BR clones, GABA_BR1a and GABA_BR1b; and humans GABA_BR clones, GABA_BR1a/b (representing a partial receptor clone) and GABA_BR1b (representing a full-length receptor clone). Amino acid sequence information, and encoding cDNA sequence information, is provided for the different GABA_BR clones.

Another GABA_BR subtype is GABA_BR2. Northern blot analysis reveals than an
 10 approximately 6.3 Kb human GABA_BR2 transcript is abundantly expressed in the human brain. Expression is not detected in the heart, placenta, lung, liver, skeletal muscle, kidney and pancreas under conditions where GABA_BR2 transcript was identified in the human brain. Within the human brain GABA_BR2 is broadly expressed at variable levels.

GABA_BR functions as a heterodimer of the subunits GABA_BR1 or GABA_BR2.
 15 (Jones *et al. Nature* 396:674-679, 1998, hereby incorporated by reference herein.)

GABA_BRs have been targeted to achieve therapeutic effects. Kerr and Ong, DDT
 1:371-380, 1996, describe different compounds indicated to be GABA_BR agonists and GABA_BR antagonists. Kerr and Ong also review therapeutic implications of affecting
 20 GABA_BR activity including, spasticity and motor control, analgesia, epilepsy, cognitive effects, psychiatric disorders, alcohol dependence and withdrawal, feeding behavior, cardiovascular and respiratory functions, and peripheral functions.

Bittiger *et al.*, *Tips* 4:391-394, 1993, review therapeutic applications of GABA_BR antagonists. Potential therapeutic applications noted by Bittiger *et al.* include cognitive
 25 processes, epilepsy, and depression.

G-Protein Fusion Receptors

Examples of some different types of G-protein fusion receptors, and advantages of some receptors, are provided below. Using the present application as guide additional G-protein receptors fusion can be constructed.

30 G-protein fusion receptors contain an intracellular domain of a receptor fused to a G-protein subunit (G). G fusions to adrenoreceptors have been reported by Bertin *et al.*, *Receptors and Channels* 5:41-51, 1997; Wise and Milligan, *Journal of Biological Chemistry* 39:24673-24678, 1997; and Bertin *et al.*, *Proc. Natl. Acad. Sci. USA* 91:8827-

8831, 1994 (each of which are hereby incorporated by reference herein). These studies were indicated to produce a functional chimeric by fusing the α_2A -adrenoreceptor to the G_{i1} , or the α_2 -adrenoreceptor to the G_s .

The G-protein fusion receptors described by the present invention include a G-protein fused to an intracellular domain, where the intracellular domain when present in a wild type receptor does not interact with that type of G-protein. Thus, the present invention also describes swapping of signals by fusing an intracellular domain to a G normally not coupled to that intracellular domain. The use of such fusion proteins, while applicable to chimeric GABA_BRs, is not limited to chimeric GABA_BRs. Indeed, such technology can be applied to receptors containing an extracellular domain, transmembrane domain and intracellular domain of a wild type receptor.

Preferred G-proteins fusion receptors contain an intracellular domain fused to a promiscuous G that couples to phospholipase C resulting in the mobilization of intracellular calcium. Increases in intracellular calcium can be conveniently measured through the use of dyes. Such techniques are well known in the art and are described, for example by Brown *et al.* U.S. Patent No. 5,688,938.

In an embodiment G-proteins fusions can also be used to decrease receptor desensitization.

Examples of promiscuous G's coupling to phospholipase C include naturally occurring G-proteins such as G_{15} and G_{16} , and chimeric G-protein such as Gqo5 and Gqi5. Gqo5 and Gqi5 are made of a Gq portion where the five amino acids at the C-terminal are from either G_o or G_i , respectively (Conklin *et al.*, *Nature* 363:274-277, 1993, hereby incorporated by reference herein). The Gq portion of such chimeric receptors provides for phospholipase C coupling while the terminal G_o or G_i portion allows the chimeric G-protein to couple to different receptor proteins that are normally involved in inhibitor effects on adenylate cyclase.

In an embodiment of the present invention the employed G-protein is from a human source or is made up of different G-protein components each from a human source.

G-proteins fusions can be created, for example, by fusing directly or indirectly the intracellular domain of a receptor protein to a polypeptide having an amino acid sequence substantially similar to G_{15} , G_{16} , Gqo5 or Gqi5. In different embodiments, the receptor

is fused directly or indirectly to a G-protein consisting of the amino acid sequence of G₁₅, G₁₆, Gqo5 or Gqi5.

The intracellular domain portion of a receptor protein fused directly or indirectly to a G-protein should be at least about 1 amino acid in length. In different embodiments the portion is at least about 10 amino acids, is at least about 50 amino acids, at least about 100 amino acids, or the full length of an intracellular domain.

The intracellular domain can be directly linked to a G-protein or can be indirectly linked through an optionally present linker. Optionally present linkers are preferably about 3 to about 30 amino acids in length. Preferred linkers are made up of alanine, glycine, or a combination thereof.

Chimeric Receptors

Examples of some different types of chimeric receptors, and advantages of some receptors, are provided below. Using the present application as guide additional chimeric receptors can be constructed.

Chimeric GABA_BR Extracellular Domain

Chimeric GABA_BRs containing a GABA_BR extracellular domain are particularly useful for studying the importance of the GABA_BR extracellular domain and assaying for compounds active at the extracellular domain. Preferably chimeric GABA_BRs containing a GABA_BR extracellular domain also contain a CaR intracellular domain.

A variety of different activities have been generally attributed to GABA_BR subtypes. (*E.g.*, Kerr and Ong, DDT 1:371-380, 1996.) Kaupmann *et al.*, *Nature* 386:239-246, 1997, report that in preliminary experiments involving GABA_BR1a they did not detect positive coupling to the adenylyl cyclase or coupling to the phospholipase effector system.

An intracellular CaR domain can be used to couple with G-proteins which activate phospholipase C and mobilize intracellular calcium. Mobilization of intracellular calcium is readily detected, for example, by fluorescent indicators of intracellular Ca²⁺.

An additional advantage of using the intracellular CaR domain is that CaR G-protein activation is not rapidly desensitized. Thus, the intracellular CaR domain can be used to produce a stronger intracellular signal than a signal produced from a receptor which is desensitized rapidly.

More preferably, the chimeric GABA_BR contains an intracellular CaR domain, and also contains either a CaR or a GABA_BR transmembrane domain. Advantages of using a CaR transmembrane domain include separating the effects occurring at a GABA_BR extracellular domain from effects occurring at a transmembrane domain; and providing additional intracellular elements, present on transmembrane intracellular loops, useful for coupling to G-protein.

A GABA_BR transmembrane domain is useful for examining whether the transmembrane GABA_BR can be targeted to affect GABA_BR activity, and obtaining compounds active at the GABA_BR transmembrane domain. For example, a transmembrane GABA_BR can be used to screen for transmembrane allosteric modulators and antagonists.

Chimeric GABA_BR Transmembrane Domain

Chimeric GABA_BRs containing a GABA_BR transmembrane are particularly useful for studying the importance of the GABA_BR transmembrane domain and assaying for compounds active at the transmembrane domain. Preferably Chimeric GABA_BRs containing a GABA_BR transmembrane domain contain an extracellular domain which is either mGluR8 or CaR, and an intracellular CaR domain.

More preferably, the chimeric GABA_BR contains an extracellular domain from either mGluR8 or CaR, a GABA_BR transmembrane, and an intracellular CaR domain. A chimeric GABA_BR containing extracellular mGluR8 or CaR domains can readily be stimulated using mGluR8 or CaR ligands.

Chimeric GABA_BR Intracellular Domain

Chimeric GABA_BRs containing a GABA_BR intracellular domain are particularly useful for studying the importance of the GABA_BR intracellular domain and assaying for compounds active at the intracellular domain. Preferably, the chimeric receptors contain an extracellular domain from either mGluR8 or CaR. The extracellular mGluR8 or CaR domains can readily be activated using mGluR8 or CaR ligands.

Receptor Domains

Domains of a G-protein fusion receptor, a chimeric receptor, and G , substantially similar to a particular sequence can be readily produced using the disclosure provided

herein in conjunction with information well known in the art. Substantially similar sequences can be obtained taking into account sequence information for a particular type of receptor obtained from different sources, different types of amino acids which are to some extent interchangeable, and the ease of experimentation with which functional
5 receptor activity can be assayed.

Substantially similar sequences includes amino acid alterations such as deletions, substitutions, additions, and amino acid modifications. A "deletion" refers to the absence of one or more amino acid residue(s) in the related polypeptide. An "addition" refers to the presence of one or more amino acid residue(s) in the related polypeptide. Additions
10 and deletions to a polypeptide may be at the amino terminus, the carboxy terminus, and/or internal. Amino acid "modification" refers to the alteration of a naturally occurring amino acid to produce a non-naturally occurring amino acid. A "substitution" refers to the replacement of one or more amino acid residue(s) by another amino acid residue(s) in the polypeptide. Derivatives can contain different combinations of alterations including more
15 than one alteration and different types of alterations.

The sequences of polypeptides can be compared from different sources to help identify variable amino acids not essential for receptor activity. For example, Figure 7 provides the rat GABA_BR1a and GABA_BR1b amino acid sequences. The rat GABA_BR1a and GABA_BR1b amino acid sequences can be compared with the human GABA_BR1a and
20 GABA_BR1b sequences to identify conserved and variable amino acids. Derivatives can then be produced where a variable amino acid is changed, and receptor activity can be readily tested.

Similarly, the amino acid sequences for CaR, mGluR8, and G-proteins from different sources are either known in the art or can readily be obtained. Examples of such
25 references are provided above.

While the effect of an amino acid change varies depending upon factors such as phosphorylation, glycosylation, intra-chain linkages, tertiary structure, and the role of the amino acid in the active site or a possible allosteric site, it is generally preferred that a substituted amino acid is from the same group as the amino acid being replaced. To some
30 extent the following groups contain amino acids which are interchangeable: the basic amino acids lysine, arginine, and histidine; the acidic amino acids aspartic and glutamic acids; the neutral polar amino acids serine, threonine, cysteine, glutamine, asparagine and, to a lesser extent, methionine; the nonpolar aliphatic amino acids glycine, alanine, valine,

isoleucine, and leucine (however, because of size, glycine and alanine are more closely related and valine, isoleucine and leucine are more closely related); and the aromatic amino acids phenylalanine, tryptophan, and tyrosine. In addition, although classified in different categories, alanine, glycine, and serine seem to be interchangeable to some extent, and cysteine additionally fits into this group, or may be classified with the polar neutral amino acids.

While proline is a nonpolar neutral amino acid, its replacement represents difficulties because of its effects on conformation. Thus, substitutions by or for proline are not preferred, except when the same or similar conformational results can be obtained.

The conformation conferring properties of proline residues may be obtained if one or more of these is substituted by hydroxyproline (Hyp).

Examples of modified amino acids include the following: altered neutral nonpolar amino acids such as α -amino acids of the formula $H_2N(CH_2)_nCOOH$ where n is 2-6, sarcosine (Sar), tbutylalanine (t-BuAla), t-butylglycine (t-BuGly), N-methyl isoleucine (N-Melle), and norleucine (Nleu); altered neutral aromatic amino acids such as phenylglycine; altered polar, but neutral amino acids such as citrulline (Cit) and methionine sulfoxide (MSO); altered neutral and nonpolar amino acids such as cyclohexyl alanine (Cha); altered acidic amino acids such as cysteic acid (Cya); and altered basic amino acids such as ornithine (Orn).

Preferred derivatives have one or more amino acid alteration(s) which do not significantly affect the receptor activity of the related receptor protein. In regions of receptor domains not necessary for receptor activity, amino acids may be deleted, added or substituted with less risk of affecting activity. In regions required for receptor activity, amino acid alterations are less preferred as there is a greater risk of affecting receptor activity.

Derivatives can be produced using standard chemical techniques and recombinant nucleic acid techniques. Modifications to a specific polypeptide may be deliberate, as through site-directed mutagenesis and amino acid substitution during solid-phase synthesis, or may be accidental such as through mutations in hosts which produce the polypeptide. Polypeptides including derivatives can be obtained using standard techniques such as those described by Sambrook *et al.*, *Molecular Cloning*, Cold Spring Harbor Laboratory Press (1989). For example, Chapter 15 of Sambrook describes procedures for site-directed mutagenesis of cloned DNA.

Receptor Nucleic Acid

G-protein fusion and chimeric receptor nucleic acid can be produced based on the information provided herein along with standard recombinant nucleic acid techniques.

- 5 Examples of references describing recombinant nucleic acid techniques include *Molecular Cloning*, Sambrook *et al.*, Cold Spring Harbor Laboratory Press (1989); and *Current Protocols in Molecular Biology*, Frederick *et al.*, John Wiley & Sons, Inc. (1995).

10 Due to the degeneracy of the genetic code different nucleic acid sequences can encode for a particular polypeptide. Thus, a large number of nucleic acids encoding for a receptor having the same amino acid sequence can be produced.

An embodiment of the present invention uses human nucleic acid encoding for the domains from CaR, GABA_BR1A, GABA_BR1B, GABA_BR2 and/or mGluR8. The amino acid sequences of different domains is provided in Figures 1-3.

Recombinant Cells

15 Nucleic acid expressing a functional G-Protein fusion or a chimeric receptor can be used to create transfected cells lines expressing such receptors. Such cell lines have a variety of uses such as being used for high-throughput screening for compounds modulating receptor activity; being used to assay binding to the receptor; and as factories to produce large amounts of a receptor.

20 A variety of cell lines can couple exogenously expressed receptors to endogenous functional responses. Cell lines such as NIH-3T3, HeLa, NG115, CHO, HEK 293 and COS7 which are expected to lack CaR, mGluR8, and GABA_BR can be tested to confirm that they lack these receptors.

25 Production of stable transfectants can be accomplished by transfection of an appropriate cell line with, for example, an expression vector such as pMSG vector, in which the coding sequence for the G-protein fusion or chimeric GABA_BR cDNA has been cloned. Expression vectors containing a promoter region, such as the mouse mammary tumor virus promoter (MMTV), drive high-level transcription of cDNAs in a variety of mammalian cells. In addition, these vectors contain genes for selecting cells stably expressing cDNA of interest. The selectable marker in the pMSG vectors encode an

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enzyme, xanthine-guanine phosphoribosyl transferase (XGPRT), conferring resistance to a metabolic inhibitor that is added to the culture to kill nontransfected cells.

The most effective method for transfection of eukaryotic cell lines with plasmid DNA varies with the given cell type. The expression construct will be introduced into cultured cells by the appropriate technique, such as Ca^{2+} phosphate precipitation, DEAE-dextran transfection, lipofection or electroporation. Expression of the receptor cDNA in cell lines can be assessed by solution hybridization and Northern blot analysis.

Binding Assays

The present invention also includes using G-protein fusion receptors or chimeric $\text{GABA}_\text{B}\text{R}$ in a binding assay. G-protein fusion receptors or chimeric $\text{GABA}_\text{B}\text{R}$ s having a particular $\text{GABA}_\text{B}\text{R}$ domain can be used, for example to facilitate obtaining compounds able to bind to that particular receptor domain; and to determine whether a compound which binds to a particular domain. For example, in a complete chimeric $\text{GABA}_\text{B}\text{R}$ containing extracellular, transmembrane, and intracellular domains, the presence of one or more domains from CaR or mGluR are useful to present $\text{GABA}_\text{B}\text{R}$ domain(s) to a binding agent in a form more like the $\text{GABA}_\text{B}\text{R}$ domain(s) in the wild type receptor compared to an incomplete $\text{GABA}_\text{B}\text{R}$ receptor fragment lacking one or more domains.

Binding assays can be carried out using techniques well known in the art. Binding assays preferably employ radiolabeled binding agents.

An example of a binding procedure is carried out by first attaching chimeric $\text{GABA}_\text{B}\text{R}$ to a solid-phase support to create an affinity matrix. The affinity matrix is then contacted with potential $\text{GABA}_\text{B}\text{R}$ binding agents. A large library of compounds may be used to determine those compounds binding to the affinity matrix. Bound compounds can be eluted from the column.

Therapeutic Modulation

As pointed out above, different types of diseases and disorders can be treated using compounds modulating CaR, mGluR, or $\text{GABA}_\text{B}\text{R}$ activity. Additionally, such compounds can be used prophylactically. Compounds modulating $\text{GABA}_\text{B}\text{R}_2$ activity can be administered to patients who would benefit from such treatment. Patients are mammals, preferably humans.

Modulators of CaR, mGluR, or GABA_BR activity can be administered to a patient using standard techniques. Techniques and formulations generally may be found in Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, 1990 (hereby incorporated by reference herein).

5 Suitable dosage forms, in part, depend upon the use or the route of entry, for example, oral, transdermal, transmucosal, or by injection (parenteral). Such dosage forms should allow the therapeutic agent to reach a target cell whether the target cell is present in a multicellular host or in culture. For example, pharmacological compounds or compositions injected into the blood stream should be soluble. Other factors are well
10 known in the art, and include considerations such as toxicity and dosage forms which retard the therapeutic agent from exerting its effect.

Therapeutic compounds can be formulated as pharmaceutically acceptable salts and complexes thereof. Pharmaceutically acceptable salts are non-toxic salts in the amounts and concentrations at which they are administered. The preparation of such salts
15 can facilitate the pharmacological use by altering the physical characteristics of the compound without preventing it from exerting its physiological effect. Useful alterations in physical properties include lowering the melting point to facilitate transmucosal administration and increasing the solubility to facilitate administering higher concentrations of the drug.

20 The pharmaceutically acceptable salt of a compound may be present as a complex. Examples of complexes include an 8-chlorotheophylline complex (analogous to, *e.g.*, dimenhydrinate:diphenhydramine 8-chlorotheophylline (1:1) complex; Dramamine) and various cyclodextrin inclusion complexes.

Pharmaceutically acceptable salts include acid addition salts such as those
25 containing sulfate, hydrochloride, fumarate, maleate, phosphate, sulfamate, acetate, citrate, lactate, tartrate, methanesulfonate, ethanesulfonate, benzenesulfonate, *p*-toluenesulfonate, cyclohexylsulfamate and quinate.

Pharmaceutically acceptable salts can be obtained from acids such as hydrochloric acid, maleic acid, sulfuric acid, phosphoric acid, sulfamic acid, acetic acid, citric acid,
30 lactic acid, tartaric acid, malonic acid, methanesulfonic acid, ethanesulfonic acid, benzenesulfonic acid, *p*-toluenesulfonic acid, cyclohexylsulfamic acid, fumaric acid, and quinic acid.

Pharmaceutically acceptable salts also include basic addition salts such as those containing benzathine, chlorprocaine, choline, diethanolamine, ethylenediamine, meglumine, procaine, aluminum, calcium, lithium, magnesium, potassium, sodium, ammonium, alkylamine, and zinc, when acidic functional groups, such as carboxylic acid or phenol are present. For example, see Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, p. 1445, 1990. Such salts can be prepared using the appropriate corresponding bases.

Carriers or excipients can also be used to facilitate administration of therapeutic agents. Examples of carriers include calcium carbonate, calcium phosphate, various sugars such as lactose, glucose, or sucrose, or types of starch, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols and physiologically compatible solvents. Examples of physiologically compatible solvents include sterile solutions of water for injection (WFI), saline solution and dextrose.

GABA_BR modulating compounds can be administered by different routes including intravenous, intraperitoneal, subcutaneous, intramuscular, oral, topical (transdermal), or transmucosal administration. For systemic administration, oral administration is preferred. For oral administration, for example, the compounds can be formulated into conventional oral dosage forms such as capsules, tablets, and liquid preparations such as syrups, elixirs, and concentrated drops.

Alternatively, injection (parenteral administration) may be used, *e.g.*, intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, compounds are formulated in liquid solutions, preferably, in physiologically compatible buffers or solutions, such as saline solution, Hank's solution, or Ringer's solution. In addition, the compounds may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms can also be produced.

Systemic administration can be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are well known in the art, and include, for example, for transmucosal administration, bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration, for example, may be through nasal sprays, rectal suppositories, or vaginal suppositories.

For topical administration, compounds can be formulated into ointments, salves, gels, or creams, as is well known in the art.

The amounts of various GABA_BR modulating compounds to be administered can be determined by standard procedures taking into account factors such as the compound IC₅₀, EC₅₀, the biological half-life of the compound, the age, size and weight of the patient, and the disease or disorder associated with the patient. The importance of these and other factors to be considered are well known to those of ordinary skill in the art. Generally, the amount is expected to preferably be between about 0.01 and 50 mg/kg of the animal to be treated.

EXAMPLES

Examples are provided below illustrating different aspects and embodiments of the present invention. The examples include techniques that can be used to produce and use G-protein fusion receptors and chimeric receptors. These examples are not intended to limit the claimed invention.

Example 1: Construction of G-Protein Fusions

This example illustrates different G-protein fusion receptor constructs and techniques used to produce different G-protein fusion receptor constructs. Numbering of nucleotide position for all the following constructs is such that nucleotide number 1 corresponds to the A of the ATG start codon of the nucleotide sequence encoding the designated protein.

I. FULL-LENGTH CONSTRUCTS

A. phCaR

The cDNA encoding the human CaR (Garrett et al., (1995) J. Biol. Chem.270:12919) is harbored in the Bluescript SK(-) plasmid (Stratagene). This construct is referred to as phCaR.

B. phmGluR2

A full length human mGluR2 cDNA was amplified from human cerebellum MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR2 cDNA sequence (Genbank Accession # 4504136). The obtained PCR fragment was

subcloned into the pT7Blue TA vector (Novagen). A Hind III-Not I fragment containing the human mGluR2 cDNA was then subcloned into the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phmGluR2.

5 C. phGα_q

A full length human Gα_q cDNA was amplified from human cerebral cortex Quick-Clone cDNA (Clontech) using PCR primers based on the human Gα_q cDNA sequence (Genbank Accession # 4504044). The obtained PCR fragment was subcloned into the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phGα_q.

10

D. phmGluR8

The cDNA encoding the full length human mGluR8 cDNA (Stormann *et al.*, U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084) is harbored in the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phmGluR8.

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E. ph8SPmGluR4

A full length human mGluR4 cDNA was amplified from human cerebellum MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR4 cDNA sequence (Genbank Accession #X80818). The obtained PCR fragment was cloned into the pT7Blue TA vector (Novagen). A 2977 bp BamHI fragment containing the human mGluR4 cDNA was then subcloned into the vector pcDNA3.1/Hygro⁺ (Invitrogen). This construct is referred to as phmGluR4.

20

Next, the predicted signal peptide of mGluR4 was replaced with the predicted signal peptide and 87 bp of 5' UTR from phmGluR8 using a recombinant PCR strategy similar to those described above. The first reaction used a phmGluR8 construct with two primers, 3.1-535F (sense 21-mer, complementary to vector sequence upstream of the hmGluR8 insert; sequence 5'-ggcattatgccaggtacatga-3'), and the hybrid primer 8/4RP (antisense 42-mer, containing 21 nucleotides complementary to human mGluR8 and 21 nucleotides complementary human mGluR4; sequence 5'-caagcctctcttcccaggcattttctccacaggtggtattgc-3'). These primers were used to amplify a 469 bp PCR fragment of human mGluR8.

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In a separate PCR reaction using phmGluR4 as template, a 472 bp fragment of

human mGluR4 was amplified using a hybrid primer 4/8RP (sense 42-mer, exactly complementary to primer 8/4RP) and oligo mG4-472R, (antisense 18-mer, complementary to the human mGluR4 cDNA; sequence 5'-ctgaagcaccgatgacac-3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers mG4-472R and 3.1-535F, and Turbo Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with NarI and NheI (New England Biolabs) and subcloned into phmGluR4 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, ph8SPmGluR4, was verified by ABI automated DNA sequence analysis. The replacement of the predicted signal peptide of mGluR4 with that of mGluR8 greatly increased the activity of this receptor in *in vitro* assays

II. $G\alpha_{qi5}$

The cDNA encoding the human $G\alpha_{qi5}$ cDNA (Conklin et al (1993) Nature 363:274-77) is harbored in the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as $G\alpha_{qi5}$. The nucleic acid and amino acid sequences for $G\alpha_{qi5}$ are provided by SEQ. ID. NOs. 28 and 29 respectively.

III. phCaR/hmGluR2

This chimera contains the extracellular domain of the human CaR and transmembrane domain and intracellular cytoplasmic tail of human mGluR2. The chimeric junction between the CaR and hmGluR2 was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, CA1156 (sense 19-mer, corresponding to nucleotides 1156-1174 of human CaR), and the hybrid primer CA/2 (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 1774-1794 of human CaR and 21 nucleotides complementary to nucleotides 1660-1680 of the human mGluR2). These primers were used to amplify a 659 bp PCR fragment of human CaR.

In a separate PCR reaction using phmGluR2 as template, a 692 bp fragment of the human mGluR2 was amplified using a hybrid primer 2/CA (sense 42-mer, exactly complementary to primer CA/2) and oligo 2-2330m, (antisense 23-mer, complementary to

nucleotides 2309-2331 of the human mGluR2 cDNA). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CA1156 and 2-2330m, and the Pfu DNA polymerase (Stratagene).

5 The resulting chimeric PCR product was digested with SexA1 (Boehringer Mannheim) and BamHI (New England Biolabs) and subcloned into phCaR digested with the same two restriction enzymes. In the final cloning step, the 3' end of human mGluR2 was subcloned into this construct using the restriction enzymes BsrGI and BamHI (both New England Biolabs). The sequence of the resultant chimeric construct,
10 phCaR/hmGluR2, was verified by ABI automated DNA sequence analysis.

IV. phCaR/hmGluR2*Gqi5

This construct contains the phCaR/hmGluR2 chimeric receptor fused to human $G\alpha_{qi5}$. A HindIII-BamHI fragment containing the phCaR/hmGluR2 construct was
15 subcloned into pcDNA3.1/Hygro(+) (Invitrogen) to aid in constructing this fusion protein.

The chimeric junction between the C-terminus of phCaR/hmGluR2 and the N-terminus of $G\alpha_{qi5}$ was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, 2-1713 (sense 21-mer, corresponding to
20 nucleotides 1710-1730 of human mGluR2) and the hybrid primer 2/Q (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 2596-2616 of human mGluR2, and 21 nucleotides complementary to nucleotides 1-21 of p $G\alpha_{qi5}$). These primers were used to amplify a 927 bp PCR fragment of phCaR/hmGluR2. In a separate PCR reaction all of $G\alpha_{qi5}$ was amplified using a hybrid primer Q/2 (sense 42-mer, exactly
25 complementary to primer 2/Q) and the and the T3 primer commercially available from Stratagene.

These two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 2-1713 and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested
30 with Bsu361 and BamHI (New England Biolabs) and subcloned into phCaR/hmGluR2 digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, phCaR/hmGluR2* $G\alpha_{qi5}$, was verified by DNA sequence analysis.

V. phmGluR2//CaR Construct

This chimera contains the extracellular and transmembrane domains of human mGluR2 linked to the intracellular cytoplasmic tail domain of the human CaR. The chimeric junction was created using three separate PCR reactions.

The first reaction used two primers, 2-1713 (sense 21-mer, corresponding to nucleotides 1710-1730 of human mGluR2, Genbank Accession # 4504136) and the hybrid primer 2/CT (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 2452 – 2472 of human mGluR2 and 21 nucleotides complementary to nucleotides 2602-2622 of the human CaR). These primers were used to amplify a 783 bp PCR fragment of human mGluR2. In a separate PCR reaction using phCaR in the BlueScript SK⁻ plasmid as template, a 750 bp fragment of the human CaR was amplified using a hybrid primer CT/2 (sense 42-mer, exactly complementary to primer 2/CT) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 2-1713 and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BsrG I and Not I (New England Biolabs) and subcloned into pmGluR2 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, pmGluR2//CaR, was verified by ABI automated DNA sequence analysis.

VI. pmGluR2//CaR*Gα_{qi5} Construct

This construct contains the hmGluR2//CaR chimeric receptor fused to human Gα_{qi5}. The chimeric junction between the C-terminus of hmGluR2//CaR and the N-terminus of Gα_{qi5} was created using a recombinant PCR strategy similar to that described above for the construction of phmGluR2//CaR.

The first reaction used two primers, CRP10A (sense 18-mer, corresponding to nucleotides 2812-2829 of phCaR) and the hybrid primer CaRQ (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 3214– 3234 phCaR, and 21 nucleotides complementary to nucleotides 1-21 of pGα_{qi5}). These primers were used to amplify a 443 bp PCR fragment of hmGluR2//CaR. In a separate PCR reaction, all of Gα_{qi5} was amplified using a hybrid primer QCaR (sense 42-mer, exactly complementary

to primer CaRQ) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CRP10A and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BstE II and Not I (New England Biolabs) and subcloned into pmGluR2//CaR digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, pmGluR2//CaR*G α _qi5, was verified by ABI automated DNA sequence analysis.

VII. Fusion Receptor Protein Linker Addition Constructs

A. phmGluR2//CaR*AAA*G α _qi5

A linker encoding three alanine residues was incorporated into the phmGluR2//CaR*G α _qi5 construct by mutagenesis (Stratagene QuickChange Mutagenesis Kit). A sense 40-mer, 2CQ+LP, contained 16 nucleotides corresponding to 3219-3234 of human CaR, followed by the 9 nucleotide sequence (GCGGCCGCC) encoding three alanine residues and a NotI restriction enzyme site, and then 15 nucleotides corresponding to nucleotides 1-15 of G α _qi5. 2CQ+LP was annealed to an antisense 40-mer, 2CQ+LM, the exact complement of 2CQ+LP. These oligos were used in the mutagenesis reaction according to the manufacturer's protocol. Restriction enzyme analysis and DNA sequence analysis confirmed the insertion of the 9 nucleotide linker (GCGGCCGCC) between the C-terminus of phmGluR2//CaR and the N-terminus of G α _qi5. This construct was designated phmGluR2//CaR*AAA*G α _qi5.

B. Human GABA_BR2*AAA*G α _qo5 and human GABA_BR1a*AAA*G α _qo5

These constructs contain the human GABA_BR2 (hGABA_BR2: Genbank Accession # AJ 012188) and human GABA_BR1a (hGABA_BR1a: Genbank Accession # AJ 012185) fused at their C-terminus to the N-terminus of human G α _qo5 (hG α _qo5: *Nature* 363:274-276, 1993). Human GABA_BR2, hGABA_BR1a, and hG α _qo5 were cloned into the plasmid pcDNA3.1/Hygro+ (Invitrogen) and are designated phGABA_BR2, phGABA_BR1a, and phG α _qo5. The first reaction used two primers, XcmI-R2 (sense 20-mer, corresponding to nucleotides 2650-2669 of phGABA_BR2) and the hybrid primer R2/Go5(-) (antisense 45-

mer, containing 18 nucleotides complementary to nucleotides 2806-2823 of phGABA_BR2 and 18 nucleotides complementary to nucleotides 1-18 of hGα_qo5). These two complementary areas flank a 9 nucleotide sequence coding for 3 alanine sequences with a unique NotI restriction site. These primers were used to amplify a 200 base-pair PCR fragment.

In a separate PCR reaction, part of hGα_qo5 was amplified using a hybrid primer R2/Gα_qo5(+) (sense 45-mer), exactly complementary to R2/Go5(-) and XbaI-Go5 primer (22-mer containing 22 nucleotides complementary to nucleotides 873-895 of hGα_qo5). These primers were used to amplify a 914 base-pair PCR product. The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers; XcmI-R2 and XbaI-Go5, and Pfu polymerase (Stratagene).

The resulting chimeric PCR product was digested with the restriction endonucleases XcmI and XbaI (New England Biolabs) and subcloned into phGABA_BR2 digested with the same two restriction enzymes. The resulting clone was then digested with HindIII and XbaI and subcloned into phGα_qo5 cut with HindIII and XbaI resulting in the chimeric hGABA_BR*AAA*Gα_qo5. The chimeric junction between the C-terminus hGABA_BR1a, the Ala linker, and the N-terminus of hGα_qo5 was created using a recombinant PCR strategy similar to those described above.

To construct hGABA_BR1a*AAA*Gqo5, the first reaction used a commercially available T7 primer (Novagen) and the NtI hGBR1 primer (CAGAGTCATGGCGGCCGCTTATAAAGCAAATGCACTCG) corresponding to nucleotide numbers 1-9 of hGα_qo5 and nucleotide numbers 2863-2883 of hGABA_BR1a.

25 C. phmGluR8//CaR*AAA*Gα_qi5

A linker encoding three alanine residues was incorporated into the phmGluR8//CaR*Gα_qi5 construct by mutagenesis (Stratagene QuickChange Mutagenesis Kit), exactly as described in Section A, above to create phmGluR2//CaR*AAA*Gα_qi5. The same primers, 2CQ+LP and 2CQ+LM, were used for this mutagenesis. Restriction enzyme analysis and DNA sequence analysis confirmed the insertion of the 9-nucleotide linker (GCGGCCGCC) between the C-terminus of phmGluR8//CaR and the N-terminus of Gα_qi5. This construct was designated phmGluR8//CaR*AAA*Gα_qi5.

D. ph8SPmGluR4//CaR*AAA*G α _qi5

This chimera contains the extracellular and transmembrane domains of the human 8SPmGluR4 construct and intracellular cytoplasmic tail of human CaR fused to G α _qi5 through the three alanine residue linker.

The chimeric junction between the human 8SPmGluR4 and hCaR was created using a recombinant PCR strategy similar to those previously described. The first reaction used two primers, mG4-2028R (sense 19-mer, corresponding to nucleotides of human 8SPmGluR4; sequence 5'-catctaccgcacatcttcgag-3'), and the hybrid primer 4CT (antisense 42-mer, containing 21 nucleotides complementary to human 8SPmGluR4 and 21 nucleotides complementary human CaR; sequence 5'-acgcacctcctcgatggtgttctgctccgggtggaagaggat-3'). These primers were used to amplify a 549 bp PCR fragment from human 8SPmGluR4.

In a separate PCR reaction, using phmGluR2//CaR*AAA*G α _qi5 as a template, a 743 bp fragment of the human CaR*AAA*G α _qi5 was amplified using the hybrid primer CT4 (sense 42-mer, exactly complementary to primer 4CT) and oligo Gaqi58R, (antisense 21-mer, complementary to G α _qi5 cDNA; sequence 5'-ctcgatctcgtcgttgatccg-3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers mG4-2028R and Gaqi58R, and Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested sequentially with KpnI and NotI (New England Biolabs) and subcloned into ph8SPmGluR4 prepared with the same two restriction enzymes. This intermediate construct was known as ph8SPmGluR4//CaR(no stop). In the final cloning step, a fragment containing the G α _qi5 cDNA was released from phmGluR8//CaR*AAA*G α _qi5 using the restriction enzymes ApaI and NotI (both New England Biolabs) and subcloned into the ph8SPmGluR4//CaR(no stop) construct, which was prepared with the same restriction enzymes. The sequence of the resultant chimeric construct, ph8SPmGluR4//CaR*AAA*G α _qi5, was verified by ABI automated DNA sequence analysis.

VIII. phmGluR8//CaR Construct

This chimera contains the extracellular and transmembrane domains of human mGluR8 linked to the intracellular cytoplasmic tail domain of the human CaR. The

chimeric junction between hmGluR8 and the CaR was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, CH5A (sense 19-mer, corresponding to nucleotides 2187-2205 of human mGluR8, Stormann *et al.*, U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084) and the hybrid primer CH5B (antisense 40-mer, containing 22 nucleotides complementary to nucleotides 2523 – 2544 of human mGluR8, and 18 nucleotides complementary to nucleotides 2602-2619 of the human CaR). These primers were used to amplify a 375 bp PCR fragment of human mGluR8. In a separate PCR reaction using phCaR in the BlueScript SK(-) plasmid as template, a 750 bp fragment of the human CaR was amplified using a hybrid primer CH5C (sense 40-mer, exactly complementary to primer CH5B) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CH5A and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BsrG I and Xba I (New England Biolabs) and subcloned into pmGluR8 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, pmGluR8//CaR, was verified by DNA sequence analysis.

IX. mGluR8//CaR*G α _{qi5} Construct

This construct contains the hmGluR8//CaR chimeric receptor fused to human G α _{qi5}. The chimeric junction between the C-terminus of hmGluR8//CaR and the N-terminus of G α _{qi5} was created using a recombinant PCR strategy similar to that described above for the construction of phmGluR2//CaR*G α _{qi5}.

The first reaction used two primers, CRP10A (sense 18-mer, corresponding to nucleotides 2812-2829 of phCaR) and the hybrid primer Gqi5/CaR (antisense 40-mer, containing 21 nucleotides complementary to nucleotides 3214-3234 phCaR, and 19 nucleotides complementary to nucleotides 1-19 of pG α _{qi5}). These primers were used to amplify a 441 bp PCR fragment of hmGluR8//CaR.

In a separate PCR reaction all of G α _{qi5} was amplified using a hybrid primer CaR/Gqi5 (sense 40-mer, exactly complementary to primer Gqi5/CaR) and the Apa I-mut primer (20-mer). The two PCR products generated from the above two reactions were

annealed together in equimolar ratios in the presence of the external primers CRP10A and Apa I-mut, and the Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with BstE II and Apa I (New England Biolabs) and subcloned into pmGluR8//CaR digested with the same two
 5 restriction enzymes. The sequence of the resultant chimeric fusion construct, pmGluR8//CaR*G α _{qi5}, was verified by DNA sequence analysis.

Example 2: Functional Expression of CaR/GABA_BR2

In vitro transcribed RNA (7 ng) encoding a chimeric CaR/GABA_BR2 (CaR
 10 extracellular and transmembrane domains, and intracellular GABA_BR2 domain) was co-injected with *in vitro* transcribed RNA (2 ng) encoding G 15 into *Xenopus* oocytes. Following a 72-hour incubation, the oocytes were voltage-clamped using standard electrophysiological techniques (Hille, B., Ionic Channels of Excitable Membranes, pp.30-33, Sinauer Associates, Inc., Sunderland, Ma., 1992). Activation of the chimeric
 15 receptor was detected by increases in the calcium-activated chloride current.

Application of the CaR activator 100 Gd³⁺, resulted in reversible, oscillatory increases in the calcium-activated chloride current as shown in Figure 8. These data demonstrate the functional response of the chimeric CaR/GABA_BR2 receptor upon activation via a site within the CaR extracellular domain. In this assay, the G 15 subunit
 20 acts to promote signal transduction through intracellular pathways that mobilize intracellular Ca⁺⁺.

Example 3: Expression of Different G-Protein Fusion Receptors

The ability of different G-protein fusions to transduce signal resulting from ligand
 25 binding is shown in Figure 15. The different G-protein fusion receptors used in this example were as follows: mGluR2//CaR*Gqi5 (SEQ. ID. NO. 37), CaR/mGluR2*Gqi5 (SEQ. ID. NO. 33), and mGluR8//CaR*Gqi5 SEQ. ID. NO. 41.

Oocytes suitable for injection were obtained from adult female *Xenopus laevis* toads using procedures described in C. J. Marcus-Sekura and M. J. M. Hitchcock,
 30 *Methods in Enzymology*, Vol. 152 (1987).

Receptor fusion cRNAs were dissolved in water and 50 nl (12.5 ng/oocyte) were injected into individual oocytes. Following injection, oocytes were incubated at 16°C in MBS containing 1 mM CaCl₂ for 2 to 7 days prior to electrophysiological recording.

Test substances were applied by superfusion at a flow rate of about 5 ml/min. Receptor fusion activation was determined by measuring the increase in calcium-activated chloride current (I_{Cl}). Increases in I_{Cl} were quantified by measuring the peak inward current stimulated by activating agent, relative to the holding current at -60 mV.

- 5 Application of 100 μ M L-glutamate elicited a response from the mGluR2//CaR*G α qi5 and mGluR8//CaR*G α qi5. Application of 100 μ M Gd³⁺ activated the CaR/mGluR2*Gqi5.

Example 4: Expression of Different G-Protein Fusion Receptors in Mammalian Cells

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HEK293 cells were transiently transfected with the p8SPhmGluR4//CaR*AAA*G α qi5 or phmGluR8//CaR*G α qi5 plasmid DNAs using the following protocol. Initially, 150 cm² tissue culture flasks containing HEK293 cells at 75% confluence were transfected with 24 μ g of plasmid DNA using Gibco BRL Life Technologies' Lipofectamine reagent. Following liposomal gene delivery the cells were

- 15 allowed to recover for 24 hours. They were then plated overnight at 100,000 cells per well in black, clear bottom, Collagen I coated 96-well plates (Becton Dickenson, Biocoat) using DMEM supplemented with 10% fetal bovine serum (Hyclone Laboratories). The cells were assayed for function 48 hours after transient tranfection.

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On the day of the assay, tissue culture medium was aspirated from the wells of a 96-well plate and 80 μ L of Assay Buffer (Assay Buffer is: 20 mM HEPES, 146 mM NaCl, 5 mM KCl, 1 mM MgCl₂, 1 mM CaCl₂, 1 mg/ml BSA, 1 mg/ml glucose, pH 7.4) supplemented with 6 μ M of the Ca²⁺-sensitive dye, Fluo-3 AM (Molecular Probes) and 0.025% Pluronic (Molecular Probes) was added to each well.

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The plate was then incubated in the dark for 1 hour at room temperature to efficiently load the cells with Fluo-3. At the end of the incubation, extracellular Fluo-3 was removed by washing the plate with Assay Buffer. Assay Buffer was added back to each well (final volume = 160 μ L) prior to beginning the assay. The plate was loaded into a fluorescence imaging plate reader (FLIPR) robotic device (Molecular Devices) with the

- 30 laser setting at 0.8 Watts. At a time of 15 seconds after initiation of the assay, 40 μ L of Assay Buffer containing 150 μ M L-AP4 was added to the 160 μ L of Assay Buffer in each well of the plate to yield a final concentration of 30 μ M L-AP4.

Relative fluorescence intensity (excitation $\lambda = 488$ nm / emission $\lambda = 510$ nm) was monitored at relevant time intervals throughout the assay period to measure L-AP4-induced receptor activation.

- 5 Other embodiments are within the following claims. Thus, while several embodiments have been shown and described, various modifications may be made, without departing from the spirit and scope of the present invention.

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Claims

1. A G-protein fusion receptor comprising

an extracellular domain comprising an extracellular domain amino acid sequence

substantially similar to either an extracellular CaR amino acid sequence, an extracellular mGluR amino acid sequence, or an extracellular GABA_B receptor amino acid sequence;

a transmembrane domain joined to the carboxy terminus of said extracellular domain, said transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to either a transmembrane CaR amino acid sequence, a transmembrane mGluR amino acid sequence, or a transmembrane GABA_B receptor amino acid sequence;

an intracellular domain joined to the carboxy terminus of said transmembrane domain comprising all or a portion of an intracellular amino acid sequence substantially similar to either an intracellular CaR amino acid sequence, an intracellular mGluR amino acid sequence, or an intracellular GABA_B receptor amino acid sequence, provided that said portion is at least about 10 amino acids;

an optionally present linker joined to the carboxy terminus of said intracellular domain; and

a G-protein joined either to said intracellular domain or to said optionally present linker, provided that said G-protein is joined to said optionally present linker when said optionally present linker is present.

2. The G-protein fusion receptor of claim 1, wherein said extracellular domain consists of said extracellular domain amino acid sequence, said transmembrane domain consists of said transmembrane domain amino acid sequence; and said intracellular domain consists of said transmembrane domain amino acid sequence.

3. The G-protein fusion receptor of claim 2, wherein said optionally present linker is present and is a polypeptide 3 to 30 amino acids in length.

4. The G-protein fusion receptor of claim 2, wherein said optionally present linker is not present.

5. 1. The G-protein fusion receptor of claim 3 or 4, wherein said G-protein is selected from the group consisting of: G₁₅, G₁₆, Gqo5, and Gqi5

5 6. The G-protein fusion of claim 5, wherein any of said CaR sequence present is a human CaR sequence, any of said mGluR sequence present is from a human mGluR, and any of said GABA_B receptor sequence present is from human mGluR.

7. A nucleic acid comprising a nucleotide sequence encoding for the G-protein fusion of any one of claims 1-6.

10 8. An expression vector comprising a nucleotide sequence encoding for the G-protein fusion of any one of claims 1-6 transcriptionally coupled to a promoter.

15 9. A recombinant cell comprising the expression vector of claim 8 and a cell wherein the G-protein fusion is expressed and is functional.

20 10. A recombinant cell produced by combining a vector comprising the nucleic acid of claim 9 and elements for introducing heterologous nucleic acid into a cell wherein the G-protein fusion receptor is expressed, and said cell.

25 11. A process for the production of a G-protein fusion receptor comprising: growing procaryotic or eukaryotic host cells comprising a nucleic acid sequence expressing the G-protein fusion receptor of any one of claims 1-6, under suitable nutrient conditions allowing for cell growth.

12. A method of measuring the ability of a compound to effect G-protein fusion activity comprising the steps of:

a) providing said compound to a cell expressing the G-protein fusion receptor of any one of claims 1-6, and

30 b) measuring the ability of said compound to affect the activity of said receptor as an indication of the ability of said compound to effect G-protein fusion receptor activity.

13. A chimeric receptor comprising

an extracellular domain comprising an extracellular domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 5;

a transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, and SEQ ID NO: 10; and

an intracellular cytoplasmic domain comprising an intracellular domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14;

wherein at least one domain is present which comprises an amino acid sequence substantially similar to a sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14; and at least one domain is present which comprises an amino acid sequence substantially similar to a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 11, and SEQ ID NO: 15.

14. The chimeric receptor of claim 13 wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 3, and 4; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 6, 7, 8, 9, and 10; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 11 and 15.

15. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 2; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 11.

16. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 3; said

transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

5 17. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence SEQ ID NO: 4; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

10 18. The chimeric receptor of claim 13, wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4 and 5; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 7, 8, and 9; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 12, 13, 14, and 15.

15 19. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 11.

20 20. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

25 21. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid

sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

22. The chimeric receptor of claim 13, wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4, and 5; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 6, 7, 8, 9, and 10; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 12, 13, and 14.

23. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 12.

24. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 12.

25. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 13.

26. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid

sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 13.

27. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 14.

28. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 14.

29. The chimeric receptor of any one of claims 13-28, wherein said receptor functional couples to a G-protein.

30. The chimeric receptor of any one of claims 13-28, wherein said chimeric receptor consists of said extracellular domain, said transmembrane domain, said intracellular domain, and an optionally present G-protein α subunit covalently joined to said intracellular domain.

31. The chimeric receptor of claim 30, wherein said chimeric receptor consists of said extracellular domain, said transmembrane domain, and said intracellular domain.

32. The chimeric receptor of claim 30, wherein said G-protein α subunit consists of the amino acid sequence of SEQ ID Nos: 16 or 17.

33. A nucleic acid comprising a nucleotide sequence encoding for the chimeric receptor of any one of claims 13-32.

34. An expression vector comprising a nucleotide sequence encoding for the chimeric receptor of any one of claims 13-32 transcriptionally coupled to a promoter.

35. A recombinant cell comprising the expression vector of claim 34 and a cell wherein the chimeric receptor is expressed and is functional.

36. A recombinant cell produced by combining a vector comprising the nucleic acid of claim 33 and elements for introducing heterologous nucleic acid into a cell wherein the chimeric receptor is expressed, and said cell.

37. A process for the production of a chimeric receptor comprising:
growing procaryotic or eukaryotic host cells comprising a nucleic acid sequence expressing the chimeric receptor of any one of claims 13-32, under suitable nutrient conditions allowing for cell growth.

38. A method of measuring the ability of a compound to effect GABA_BR or mGluR activity comprising the steps of:

a) providing said compound to a cell expressing the chimeric receptor of any one of claims 13-32, and

b) measuring the ability of said compound to affect the activity of said receptor as an indication of the ability of said compound to effect GABA_BR or mGluR activity.

39. The method of claim 38, wherein said method measures activity at a GABA_BR.

40. The method of claim 38, wherein said method measures activity at a mGluR.

41. A fusion receptor polypeptide comprising a receptor and a G-protein α subunit, wherein said G-protein α subunit is fused to the intracellular domain of said receptor, provided that said receptor is not an adrenoreceptor.

ABSTRACT

The present invention features G-protein fusion receptors and chimeric GABA_B receptors (GABA_BRs), nucleic acid encoding such receptors, and the use of such receptors and nucleic acid. G-protein fusion receptors comprise at least one domain from a CaR, a mGluR, and/or a GABA_B receptor fused directly or through a linker to a guanine nucleotide-binding protein (G-protein). Chimeric GABA_BRs comprise at least one of a GABA_BR extracellular domain, a GABA_BR transmembrane domain, or a GABA_BR intracellular domain and one or more domains from a mGluR subtype 8 (mGluR8) and/or a CaR.

ClustalW Formatted Alignments

```
SEQ ID 1  M A F Y S C C W V L L A L T W H T S A Y G P D Q R
SEQ ID 2  M L L L L L L A P L F L R P P G A G G A Q T P N A
SEQ ID 3  M G P G A P F A R V G W P L P L L V V M A A G V A
SEQ ID 4  M A S P R S S G Q P G P X P P P P P P A R L L L
SEQ ID 5  M V C E G K R S A S C P C F F L L T A K F Y W I L
```

```
SEQ ID 1  A Q K K G D I I L G G L F P I H F G V A A K D Q D
SEQ ID 2  T S E G C Q I I H P P W E G G I R Y R G L T R D Q
SEQ ID 3  P V W A S H S P H L P R P H S R V P P H P S S E R
SEQ ID 4  L L L L P L L L P L A P G A W G W A R G A P R P P
SEQ ID 5  T M M Q R T H S Q E Y A H S I R V D G D I I L G G
```

```
SEQ ID 1  L K S R P E S V E C I R Y N F R G F R W L Q A M I
SEQ ID 2  V K A I N F L P V D Y E I E Y V C R G E R E V V G
SEQ ID 3  R A V Y I G A L F P M S G G W P G G Q A C Q P A V
SEQ ID 4  P S S P P L S I M G L M P L T K E V A K G S I G R
SEQ ID 5  L F P V H A K G E R G V P C G E L K K E K G I H R
```

```
SEQ ID 1  F A I E E I N S S P A L L P N L T L G Y R I F D T
SEQ ID 2  P K V R K C L A N G S W T D M D T P S R C V R I C
SEQ ID 3  E M A L E D V N S R R D I L P D Y E L K L I H H D
SEQ ID 4  G V L P A V E L A I E Q I R N E S L L R P Y F L D
SEQ ID 5  L E A M L Y A I D Q I N K D P D L L S N I T L G V
```

```
SEQ ID 1  C N T V S K A L E A T L S F V A Q N K I D S L N L
SEQ ID 2  S K S Y L T L E N G K V F L T G G D L P A L D G A
SEQ ID 3  S K C D P G Q A T K Y L Y E L L Y N D P I K I I L
SEQ ID 4  L R L Y D T E C D N A K G L K A F Y D A I K Y G P
SEQ ID 5  R I L D T C S R D T Y A L E Q S L T F V Q A L I E
```

```
SEQ ID 1  D E F C N C S E H I P S T I A V V G A T G S G V S
SEQ ID 2  R V D F R C D P D F H L V G S S R S I C S Q G Q W
SEQ ID 3  M P G C S S V S T L V A E A A R M W N L I V L S Y
SEQ ID 4  N H L M V F G G V C P S V T S I I A E S L Q G W N
SEQ ID 5  K D A S D V K C A N G D P P I F T K P D K I S G V
```

```
SEQ ID 1  T A V A N L L G L F Y I P Q V S Y A S S S R L L S
SEQ ID 2  S T P K P H C Q V N R T P H S E R R A V Y I G A L
SEQ ID 3  G S S S P A L S N R Q R F P T F F R T H P S A T L
SEQ ID 4  L V Q L S F A A T T P V L A D K K K Y P Y F F R T
SEQ ID 5  I G A A A S S V S I M V A N I L R L F K I P Q I S
```

Figure 1a

SEQ ID 1 N K N Q F K S F L R T I P N D E H Q A T A M A D I
 SEQ ID 2 F P M S G G W P G G Q A C Q P A V E M A L E D V N
 SEQ ID 3 H N P T R V K L F E K W G W K K I A T I Q Q T T E
 SEQ ID 4 V P S D N A V N P A I L K L L K H Y Q W K R V G T
 SEQ ID 5 Y A S T A P E L S D N T R Y D F F S R V V P P D S

SEQ ID 1 I E Y F R W N W V G T I A A D D D Y G R P G I E K
 SEQ ID 2 S R R D I L P D Y E L K L I H H D S K C D P G Q A
 SEQ ID 3 V F T S T L D D L E E R V K E A G I E I T F R Q S
 SEQ ID 4 L T Q D V Q R F S E V R N D L T G V L Y G E D I E
 SEQ ID 5 Y Q A Q A M V D I V T A L G W N Y V S T L A S E G

SEQ ID 1 F R E E A E E R D I C I D F S E L I S Q Y S D E E
 SEQ ID 2 T K Y L Y E L L Y N D P I K I I L M P G C S S V S
 SEQ ID 3 F F S D P A V P V K N L K R Q D A R I I V G L F Y
 SEQ ID 4 I S D T E S F S N D P C T S V K K L K G N D V R I
 SEQ ID 5 N Y G E S G V E A F T Q I S R E I G G V C I A Q S

SEQ ID 1 E I Q H V V E V I Q N S T A K V I V V F S S G P D
 SEQ ID 2 T L V A E A A R M W N L I V L S Y G S S S P A L S
 SEQ ID 3 E T E A R K V F C E V Y K E R L F G K K Y V W F L
 SEQ ID 4 I L G Q F D Q N M A A K V F C C A Y E E N M Y G S
 SEQ ID 5 Q K I P R E P R P G E F E K I I K R L L E T P N A

SEQ ID 1 L E P L I K E I V R R N I T G K I W L A S E A W A
 SEQ ID 2 N R Q R F P T F F R T H P S A T L H N P T R V K L
 SEQ ID 3 I G W Y A D N W F K I Y D P S I N C T V D E M T E
 SEQ ID 4 K Y Q W I I P G W Y E P S W W E Q V H T E A N S S
 SEQ ID 5 R A V I M F A N E D D I R R I L E A A K K L N Q S

SEQ ID 1 S S S L I A M P Q Y F H V V G G T I G F A L K A G
 SEQ ID 2 F E K W G W K K I A T I Q Q T T E V F T S T L D D
 SEQ ID 3 A V E G H I T T E I V M L N P A N T R S I S N M T
 SEQ ID 4 R C L R K N L L A A M E G Y I G V D F E P L S S K
 SEQ ID 5 G H F L W I G S D S W G S K I A P V Y Q Q E E I A

SEQ ID 1 Q I P G F R E F L K K V H P R K S V H N G F A K E
 SEQ ID 2 L E E R V K E A G I E I T F R Q S F F S D P A V P
 SEQ ID 3 S Q E F V E K L T K R L K R H P E E T G G F Q E A
 SEQ ID 4 Q I K T I S G K T P Q Q Y E R E Y N N K R S G V G
 SEQ ID 5 E G A V T I L P K R A S I D G F D R Y F R S R T L

Figure 1b

SEQ ID 1 F W E E T F N C H L Q E G A K G P L P V D T F L R
 SEQ ID 2 V K N L K R Q D A R I I V G L F Y E T E A R K V F
 SEQ ID 3 P L A Y D A I W A L A L A L N K T S G G G G R S G
 SEQ ID 4 P S K F H G Y A Y D G I W V I A K T L Q R A M E T
 SEQ ID 5 A N N R R N V W F A E F W E E N F G C K L G S H G

SEQ ID 1 G H E E S G D R F S N S S T A F R P L C T G D E N
 SEQ ID 2 C E V Y K E R L F G K K Y V W F L I G W Y A D N W
 SEQ ID 3 V R L E D F N Y N N Q T I T D Q I Y R A M N S S S
 SEQ ID 4 L H A S S R H Q R I Q D F N Y T D H T L G R I I L
 SEQ ID 5 K R N S H I K K C T G L E R I A R D S S Y E Q E G

SEQ ID 1 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y
 SEQ ID 2 F K I Y D P S I N C T V D E M T E A V E G H I T T
 SEQ ID 3 F E G V S G H V V F D A S G S R M A W T L I E Q L
 SEQ ID 4 N A M N E T N F F G V T G Q V V F R N G E R M G T
 SEQ ID 5 K V Q F V I D A V Y S M A Y A L H N M H K D L C P

SEQ ID 1 S I A H A L Q D I Y T C L P G R G L F T N G S C A
 SEQ ID 2 E I V M L N P A N T R S I S N M T S Q E F V E K L
 SEQ ID 3 Q G G S Y K K I G Y Y D S T K D D L S W S K T D K
 SEQ ID 4 I K F T Q F Q D S R E V K V G E Y N A V A D T L E
 SEQ ID 5 G Y I G L C P R M S T I D G K E L L G Y I R A V N

SEQ ID 1 D I K K V E A W Q V L K H L R H L N F T N N M G E
 SEQ ID 2 T K R L K R H P E E T G G F Q E A P L A Y D A I W
 SEQ ID 3 W I G G S P P A D Q T L V I K T F R F L S Q K
 SEQ ID 4 I I N D T I R F Q G S E P P K D K T I I L E Q L R
 SEQ ID 5 F N G S A G T P V T F N E N G D A P G R Y D I F Q

SEQ ID 1 Q V T F D E C G D L V G N Y S I I N W H L S P E D
 SEQ ID 2 A L A L A L N K T S G G G G R S G V R L E D F N Y
 SEQ ID 3
 SEQ ID 4 K I S L P
 SEQ ID 5 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E

SEQ ID 1 G S I V F K E V G Y Y N V Y A K K G E R L F I N E
 SEQ ID 2 N N Q T I T D Q I Y R A M N S S S F E G V S G H V
 SEQ ID 3
 SEQ ID 4
 SEQ ID 5 D M Q W A H R E H T H P A S V C S L P C K P G E R

Figure 1c

SEQ ID 1 E K I L W S G F S R E V P F S N C S R D C L A G T
SEQ ID 2 V F D A S G S R M A W T L I E Q L Q G G S Y K K I
SEQ ID 3
SEQ ID 4
SEQ ID 5 K K T V K G V P C C W H C E R C E G Y N Y Q V D E

SEQ ID 1 R K G I I E G E P T C C F E C V E C P D G E Y S D
SEQ ID 2 G Y Y D S T K D D L S W S K T D K W I G G S P P A
SEQ ID 3
SEQ ID 4
SEQ ID 5 L S C E L C P L D Q R P N M N R T G C Q L I P I I

SEQ ID 1 E T D A S A C N K C P D D F W S N E N H T S C I A
SEQ ID 2 D Q T L V I K T F R F L S Q K
SEQ ID 3
SEQ ID 4
SEQ ID 5 K L E W H S P W

SEQ ID 1 K E I E F L S W T E P F
SEQ ID 2
SEQ ID 3
SEQ ID 4
SEQ ID 5

Figure 1d

FIGURE 2a

SEQ ID 6 G I A L T L F A V L G I F L T A F V L G V F I K F R N T P I
SEQ ID 7 L F I S V S V L S S L G I V L A V V C L S F N I Y N S H V R
SEQ ID 8 L F I S V S V L S S L G I V L A V V C L S F N I Y N S H V R
SEQ ID 9 L Y S I L S A L T I L G M I M A S A F L F F N I K N R N Q K
SEQ ID 10 A V V P V F V A I L G I I A T T F V I V T F V R Y N D T P I

SEQ ID 6 V K A T N R E L S Y L L L F S L L C C F S S S L F F I G E P
SEQ ID 7 Y I Q N S Q P N L N N L T A V G C S L A L A A V F P L G L D
SEQ ID 8 Y I Q N S Q P N L N N L T A V G C S L A L A A V F P L G L D
SEQ ID 9 L I K M S S P Y M N N L I I L G G M L S Y A S I F L F G L D
SEQ ID 10 V R A S G R E L S Y V L L T G I F L C Y S I T F L M I A A P

SEQ ID 6 Q D W T C R L R Q P A F G I S F V L C I S C I L V K T N R V
SEQ ID 7 G Y H I G R N Q F P F V C Q A R L W L L G L G F S L G Y G S
SEQ ID 8 G Y H I G R N Q F P F V C Q A R L W L L G L G F S L G Y G S
SEQ ID 9 G S F V S E K T F E T L C T V R T W I L T V G Y T T A F G A
SEQ ID 10 D T I I C S F R R V F L G L G M C F S Y A A L L T K T N R I

SEQ ID 6 L L V F E A K I P T S F H R K W W G L N L Q F L L V F L C T
SEQ ID 7 M F T K I W W V H T V F T K K E E K K E W R K T L E P W K L
SEQ ID 8 M F T K I W W V H T V F T K K E E K K E W R K T L E P W K L
SEQ ID 9 M F A K T W R V H A I F K N V K M K K K I I K D Q K L L V I
SEQ ID 10 H R I F E Q G K K S V T A P K F I S P A S Q L V I T F S L I

SEQ ID 6 F M Q I V I C V I W L Y T A P P S S Y R N Q E L E D E I I F
SEQ ID 7 Y A T V G L L V G M D V L T L A I W Q I V D P L H R T I E T
SEQ ID 8 Y A T V G L L V G M D V L T L A I W Q I V D P L H R T I E T
SEQ ID 9 V G G M L L I D L C I L I C W Q A V D P L R R T V E K Y S M
SEQ ID 10 S V Q L L G V F V W F V V D P P H I I I D Y G E Q R T L D P

SEQ ID 6 I T C H E G S L M A L G F L I G Y T C L L A A I C F F F A F
SEQ ID 7 F A K E E P K E D I D V S I L P Q L E H C S S R K M N T W L
SEQ ID 8 F A K E E P K E D I D V S I L P Q L E H C S S R K M N T W L
SEQ ID 9 E P D P A G R D I S I R P L L E H C E N T H M T I W L G I V
SEQ ID 10 E K A R G V L K C D I S D L S L I C S L G Y S I L L M V T C

SEQ ID 6 K S R K L P E N F N E A K F I T F S M L I F F I V W I S F I
SEQ ID 7 G I F Y G Y K G L L L L L G I F L A Y E T K S V S T E K I N
SEQ ID 8 G I F Y G Y K G L L L L L G I F L A Y E T K S V S T E K I N
SEQ ID 9 Y A Y K G L L M L F G C F L A W E T R N V S I P A L N D S K
SEQ ID 10 T V Y A I K T R G V P E T F N E A K P I G F T M Y T T C I I

FIGURE 2L

SEQ ID 6 P A Y A S T Y G K F V S A V E V I A I L A A S F G L L A C I
SEQ ID 7 D H R A V G M A I Y N V A V L C L I T A P V T M I L S S Q Q
SEQ ID 8 D H R A V G M A I Y N V A V L C L I T A P V T M I L S S Q Q
SEQ ID 9 Y I G M S V Y N V G I M C I I G A A V S F L T R D Q P N V Q
SEQ ID 10 W L A F I P I F F G T A Q S A E K M Y I Q T T T L T V S M S

SEQ ID 6 F F N K I Y I I L F
SEQ ID 7 D A A F A F A S L A I V F S S Y I T L V V L F V P K M
SEQ ID 8 D A A F A F A S L A I V F S S Y I T L V V L F V P K M
SEQ ID 9 F C I V A L V I I F C S T I T L C L V F V P K L
SEQ ID 10 L S A S V S L G M L Y M P K V Y I I I F

FIGURE 3a

SEQ ID 11 K P S R N T I E E V R C S T A A H A F K V A A R A T L R R S
SEQ ID 12 R R L I T R G E W Q S E A Q D T M K T G S S T N N N E E E K
SEQ ID 13 R R L I T R G E W Q S E A Q D T M K T G S S T N N N E E E K
SEQ ID 14 I T L R T N P D A A T Q N R R F Q F T Q N Q K K E D S K T S
SEQ ID 15 H P E Q N V Q K R K R S F K A V V T A A T M Q S K L I Q K G

SEQ ID 11 N V S R K R S S S L G G S T G S T P S S S I S S K S N S E D
SEQ ID 12 S R L L E K E N R E L E K I I A E K E E R V S E L R H Q L Q
SEQ ID 13 S R L L E K E N R E L E K I I A E K E E R V S E L R H Q L Q
SEQ ID 14 T S V T S V N Q A S T S R L E G L Q S E N H R L R M K I T E
SEQ ID 15 N D R P N G E V K S E L C E S L E T N S K S S V E F P M V K

SEQ ID 11 P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L T L P Q
SEQ ID 12 S R Q Q L R S R R H P P T P P E P S G G L P R G P P E P P D
SEQ ID 13 S R Q Q L R S R R H P P T P P E P S G G L P R G P P E P P D
SEQ ID 14 L D K D L E E V T M Q L Q D T P E K T T Y I K Q N H Y Q E L
SEQ ID 15 S G S T S

SEQ ID 11 Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S F D E P
SEQ ID 12 R L S C D G S R V H L L Y K
SEQ ID 13 R L S C D G S R V H L L Y K
SEQ ID 14 N D I L N L G N F T E S T D G G K A I L K N H L D Q N P Q L
SEQ ID 15

SEQ ID 11 Q K N A M A H G N S T H Q N S L E A Q K S S D T L T R H Q P
SEQ ID 12
SEQ ID 13
SEQ ID 14 Q W N T T E P S R T C K D P I E D I N S P E H I Q R R L S L
SEQ ID 15

SEQ ID 11 L L P L Q C G E T D L D L T V Q E T G L Q G P V G G D Q R P
SEQ ID 12
SEQ ID 13
SEQ ID 14 Q L P I L H H A Y L P S I G G V D A S C V S P C V S P T A S
SEQ ID 15

SEQ ID 11 E V E D P E E L S P A L V V S S S Q S F V I S G G G S T V T
SEQ ID 12
SEQ ID 13
SEQ ID 14 P R H R H V P P S F R V M V S G L
SEQ ID 15

FIGURE 3.

SEQ ID 11 E N V V N S
SEQ ID 12
SEQ ID 13
SEQ ID 14
SEQ ID 15

FIGURE 4a

SEQ. ID. NO. 16 M A R S L T W G C C P W C L T E E E K T A A R I D Q E I N R
SEQ. ID. NO. 17 M A R S L T W R C C P W C L T E D E K A A A R V D Q E I N R

SEQ. ID. NO. 16 I L L E Q K K Q E R E E L K L L L L G P G E S G K S T F I K
SEQ. ID. NO. 17 I L L E Q K K Q D R G E L K L L L L G P G E S G K S T F I K

SEQ. ID. NO. 16 Q M R I I H G V G Y S E E D R R A F R L L I Y Q N I F V S M
SEQ. ID. NO. 17 Q M R I I H G A G Y S E E E R K G F R P L V Y Q N I F V S M

SEQ. ID. NO. 16 Q A M I D A M D R L Q I P F S R P D S K Q H A S L V M T Q D
SEQ. ID. NO. 17 R A M I E A M E R L Q I P F S R P E S K H H A S L V M S Q D

SEQ. ID. NO. 16 P Y K V S T F E K P Y A V A M Q Y L W R D A G I R A C Y E R
SEQ. ID. NO. 17 P Y K V T T F E K R Y A A A M Q W L W R D A G I R A C Y E R

SEQ. ID. NO. 16 R R E F H L L D S A V Y Y L S H L E R I S E D S Y I P T A Q
SEQ. ID. NO. 17 R R E F H L L D S A V Y Y L S H L E R I T E E G Y V P T A Q

SEQ. ID. NO. 16 D V L R S R M P T T G I N E Y C F S V K K T K L R I V D V G
SEQ. ID. NO. 17 D V L R S R M P T T G I N E Y C F S V Q K T N L R I V D V G

SEQ. ID. NO. 16 G Q R S E R R K W I H C F E N V I A L I Y L A S L S E Y D Q
SEQ. ID. NO. 17 G Q K S E R K K W I H C F E N V I A L I Y L A S L S E Y D Q

SEQ. ID. NO. 16 C L E E N D Q E N R M E E S L A L F S T I L E L P W F K S T
SEQ. ID. NO. 17 C L E E N N Q E N R M K E S L A L F G T I L E L P W F K S T

SEQ. ID. NO. 16 S V I L F L N K T D I L E D K I H T S H L A T Y F P S F Q G
SEQ. ID. NO. 17 S V I L F L N K T D I L E E K I P T S H L A T Y F P S F Q G

SEQ. ID. NO. 16 P R R D A E A A K S F I L D M Y A R V Y A S C A E P Q D G G
SEQ. ID. NO. 17 P K Q D A E A A K R F I L D M Y T R M Y T G C V D G P E G S

SEQ. ID. NO. 16 R K G S R A R R F F A H F T C A T D T Q S V R S V F K D V R
SEQ. ID. NO. 17 K K G A R S R R L F S H Y T C A T D T Q N I R K V F K D V R

FIGURE 4b

SEQ. ID. NO. 16 D S V L A R Y L D E I N L L
SEQ. ID. NO. 17 D S V L A R Y L D E I N L L

ClustalW Formatted Alignments

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SEQ. ID. NO. 18  A T G G C A T T T T A T A G C T G C T G C T G G G
SEQ. ID. NO. 19  A T G T T G C T G C T G C T A C T G G C G C
SEQ. ID. NO. 20  A T G G G G C C C G G G G C C C C T T T T G C C C
SEQ. ID. NO. 21  A T G G C T T C C C C G C G G A G C T C C G G G C
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SEQ. ID. NO. 18  T C C T C T T G G C A C T C A C C T G G C A C A C
SEQ. ID. NO. 19  C A C T C T T C C T C C G C C C C C C G G G C G C
SEQ. ID. NO. 20  G G G T G G G G T G G C C A C T G C C G C T T C T
SEQ. ID. NO. 21  A G C C C G G G C C G C - G C C G C C G C C G C C
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SEQ. ID. NO. 18  C T C T G C C T A C G G G C C A G A C C A G C G A
SEQ. ID. NO. 19  G G G C G G G G C G C A G A C C C C C A A C G C C
SEQ. ID. NO. 20  G G T T G T G A T G G C G G C A G G G G T G G C T
SEQ. ID. NO. 21  A C C G C C G C C C G C G C G C C T G C T A C T G
```

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SEQ. ID. NO. 18  G C C C A A A A G A A G G G G G A C A T T A T C C
SEQ. ID. NO. 19  A C C T C A G A A G G T T G C C A G A T C A T A C
SEQ. ID. NO. 20  C C G G T G T G G G C C T C C C A C T C C C C C C
SEQ. ID. NO. 21  C T A C T G C T G C T G C C G C T G C T G C T G C
```

```
SEQ. ID. NO. 18  T T G G G G G G C T C T T T C C T A T T C A T T T
SEQ. ID. NO. 19  A C C C G C C C T G G G A A G G G G G C A T C A G
SEQ. ID. NO. 20  A T C T C C C G C G G C C T C A C T C G C G G G T
SEQ. ID. NO. 21  C T C T G G C G C C C G G G G C C T G G G G C T G
```

```
SEQ. ID. NO. 18  T G G A G T A G C A G C T A A A G A T C A A G A T
SEQ. ID. NO. 19  G T A C C G G G G C C T G A C T C G G G A C C A G
SEQ. ID. NO. 20  C C C C C G C A C C C C T C C T C A G A A C G G
SEQ. ID. NO. 21  G G C G C G G G G C G C C C C C C G G C C G C C G
```

```
SEQ. ID. NO. 18  C T C A A A T C A A G G C C G G A G T C T G T G G
SEQ. ID. NO. 19  G T G A A G G C T A T C A A C T T C C T G C C A G
SEQ. ID. NO. 20  C G C G C A G T G T A C A T C G G G G C A C T G T
SEQ. ID. NO. 21  C C C A G C A G C C C G C C G C T C T C C A T C A
```

```
SEQ. ID. NO. 18  A A T G T A T C A G G T A T A A T T T C C G T G G
SEQ. ID. NO. 19  T G G A C T A T G A G A T T G A G T A T G T G T G
SEQ. ID. NO. 20  T T C C C A T G A G C G G G G G C T G G C C A G G
SEQ. ID. NO. 21  T G G G C C T C A T G C C G C T C A C C A A G G A
```

Figure 5a

SEQ. ID. NO. 18 G T T T C G C T G G T T A C A G G C T A T G A T A
 SEQ. ID. NO. 19 C C G G G G G G A G C G C G A G G T G G T G G G G
 SEQ. ID. NO. 20 G G G C C A G G C C T G C C A G C C C G C G G T G
 SEQ. ID. NO. 21 G G T G G C C A A G G G C A G C A T C G G G C G C

SEQ. ID. NO. 18 T T T G C C A T A G A G G A G A T A A A C A G C A
 SEQ. ID. NO. 19 C C C A A G G T C C G C A A G T G C C T G G C C A
 SEQ. ID. NO. 20 G A G A T G G C G C T G G A G G A C G T G A A T A
 SEQ. ID. NO. 21 G G T G T G C T C C C C G C C G T G G A A C T G G

SEQ. ID. NO. 18 G C C C A G C C C T T C T T C C C A A C T T G A C
 SEQ. ID. NO. 19 A C G G C T C C T G G A C A G A T A T G G A C A C
 SEQ. ID. NO. 20 G C C G C A G G G A C A T C C T G C C G G A C T A
 SEQ. ID. NO. 21 C C A T C G A G C A G A T C C G C A A C G A G T C

SEQ. ID. NO. 18 G C T G G G A T A C A G G A T A T T T G A C A C T
 SEQ. ID. NO. 19 A C C C A G C C G C T G T G T C C G A A T C T G C
 SEQ. ID. NO. 20 T G A G C T C A A G C T C A T C C A C C A C G A C
 SEQ. ID. NO. 21 A C T C C T G C G C C C C T A C T T C C T C G A C

SEQ. ID. NO. 18 T G C A A C A C C G T T T C T A A G G C C T T G G
 SEQ. ID. NO. 19 T C C A A G T C T T A T T T G A C C C T G G A A A
 SEQ. ID. NO. 20 A G C A A G T G T G A T C C A G G C C A A G C C A
 SEQ. ID. NO. 21 C T G C G G C T C T A T G A C A C G G A G T G C G

SEQ. ID. NO. 18 A A G C C A C C C T G A G T T T T G T T G C T C A
 SEQ. ID. NO. 19 A T G G G A A G G T T T T C C T G A C G G G T G G
 SEQ. ID. NO. 20 C C A A G T A C C T A T A T G A G C T G C T C T A
 SEQ. ID. NO. 21 A C A A C G C A A A A G G G T T G A A A G C C T T

SEQ. ID. NO. 18 A A A C A A A A T T G A T T C T T T G A A C C T T
 SEQ. ID. NO. 19 G G A C C T C C C A G C T C T G G A C G G A G C C
 SEQ. ID. NO. 20 C A A C G A C C C T A T C A A G A T C A T C C T T
 SEQ. ID. NO. 21 C T A C G A T G C A A T A A A A T A C G G G C C G

SEQ. ID. NO. 18 G A T G A G T T C T G C A A C T G C T C A G A G C
 SEQ. ID. NO. 19 C G G G T G G A T T T C C G G T G T G A C C C C G
 SEQ. ID. NO. 20 A T G C C T G G C T G C A G C T C T G T C T C C A
 SEQ. ID. NO. 21 A A C C A C T T G A T G G T G T T T G G A G G C G

Figure 5b

SEQ. ID. NO. 18 A C A T T C C C T C T A C G A T T G C T G T G G T
 SEQ. ID. NO. 19 A C T T C C A T C T G G T G G G C A G C T C C C G
 SEQ. ID. NO. 20 C G C T G G T G G C T G A G G C T G C T A G G A T
 SEQ. ID. NO. 21 T C T G T C C A T C C G T C A C A T C C A T C A T

SEQ. ID. NO. 18 G G G A G C A A C T G G C T C A G G C G T C T C C
 SEQ. ID. NO. 19 G A G C A T C T G T A G T C A G G G C C A G T G G
 SEQ. ID. NO. 20 G T G G A A C C T C A T T G T G C T T T C C T A T
 SEQ. ID. NO. 21 T G C A G A G T C C C T C C A A G G C T G G A A T

SEQ. ID. NO. 18 A C G G C A G T G G C A A A T C T G C T G G G G C
 SEQ. ID. NO. 19 A G C A C C C C C A A G C C C C A C T G C C A G G
 SEQ. ID. NO. 20 G G C T C C A G C T C A C C A G C C C T G T C A A
 SEQ. ID. NO. 21 C T G G T G C A G C T T T C T T T T G C T G C A A

SEQ. ID. NO. 18 T C T T C T A C A T T C C C C A G G T C A G T T A
 SEQ. ID. NO. 19 T G A A T C G A A C G C C A C A C T C A G A A C G
 SEQ. ID. NO. 20 A C C G G C A G C G T T T C C C C A C T T T C T T
 SEQ. ID. NO. 21 C C A C G C C T G T T C T A G C C G A T A A G A A

SEQ. ID. NO. 18 T G C C T C C T C C A G C A G A C T C C T C A G C
 SEQ. ID. NO. 19 G C G C G C A G T G T A C A T C G G G G C A C T G
 SEQ. ID. NO. 20 C C G A A C G C A C C C A T C A G C C A C A C T C
 SEQ. ID. NO. 21 A A A A T A C C C T T A T T T C T T T C G G A C C

SEQ. ID. NO. 18 A A C A A G A A T C A A T T C A A G T C T T T C C
 SEQ. ID. NO. 19 T T T C C C A T G A G C G G G G G C T G G C C A G
 SEQ. ID. NO. 20 C A C A A C C C T A C C C G C G T G A A A C T C T
 SEQ. ID. NO. 21 G T C C C A T C A G A C A A T G C G G T G A A T C

SEQ. ID. NO. 18 T C C G A A C C A T C C C C A A T G A T G A G C A
 SEQ. ID. NO. 19 G G G G C C A G G C C T G C C A G C C C G C G G T
 SEQ. ID. NO. 20 T T G A A A A G T G G G G C T G G A A G A A G A T
 SEQ. ID. NO. 21 C A G C C A T T C T G A A G T T G C T C A A G C A

SEQ. ID. NO. 18 C C A G G C C A C T G C C A T G G C A G A C A T C
 SEQ. ID. NO. 19 G G A G A T G G C G C T G G A G G A C G T G A A T
 SEQ. ID. NO. 20 T G C T A C C A T C C A G C A G A C C A C T G A G
 SEQ. ID. NO. 21 C T A C C A G T G G A A G C G C G T G G G C A C G

Figure 5c

SEQ. ID. NO. 18 A T C G A G T A T T T C C G C T G G A A C T G G G
 SEQ. ID. NO. 19 A G C C G C A G G G A C A T C C T G C C G G A C T
 SEQ. ID. NO. 20 G T C T T C A C T T C G A C T C T G G A C G A C C
 SEQ. ID. NO. 21 C T G A C G C A A G A C G T T C A G A G G T T C T

SEQ. ID. NO. 18 T G G G C A C A A T T G C A G C T G A T G A C G A
 SEQ. ID. NO. 19 A T G A G C T C A A G C T C A T C C A C C A C G A
 SEQ. ID. NO. 20 T G G A G G A A C G A G T G A A G G A G G C T G G
 SEQ. ID. NO. 21 C T G A G G T G C G G A A T G A C C T G A C T G G

SEQ. ID. NO. 18 C T A T G G G C G G C C G G G G A T T G A G A A A
 SEQ. ID. NO. 19 C A G C A A G T G T G A T C C A G G C C A A G C C
 SEQ. ID. NO. 20 A A T T G A G A T T A C T T T C C G C C A G A G T
 SEQ. ID. NO. 21 A G T T C T G T A T G G C G A G G A C A T T G A G

SEQ. ID. NO. 18 T T C C G A G A G G A A G C T G A G G A A A G G G
 SEQ. ID. NO. 19 A C C A A G T A C C T A T A T G A G C T G C T C T
 SEQ. ID. NO. 20 T T C T T C T C A G A T C C A G C T G T G C C C G
 SEQ. ID. NO. 21 A T T T C A G A C A C C G A G A G C T T C T C C A

SEQ. ID. NO. 18 A T A T C T G C A T C G A C T T C A G T G A A C T
 SEQ. ID. NO. 19 A C A A C G A C C C T A T C A A G A T C A T C C T
 SEQ. ID. NO. 20 T C A A A A A C C T G A A G C G C C A G G A T G C
 SEQ. ID. NO. 21 A C G A T C C C T G T A C C A G T G T C A A A A A

SEQ. ID. NO. 18 C A T C T C C C A G T A C T C T G A T G A G G A A
 SEQ. ID. NO. 19 T A T G C C T G G C T G C A G C T C T G T C T C C
 SEQ. ID. NO. 20 C C G A A T C A T C G T G G G A C T T T T C T A T
 SEQ. ID. NO. 21 G C T G A A G G G G A A T G A T G T G C G G A T C

SEQ. ID. NO. 18 G A G A T C C A G C A T G T G G T A G A G G T G A
 SEQ. ID. NO. 19 A C G C T G G T G G C T G A G G C T G C T A G G A
 SEQ. ID. NO. 20 G A G A C T G A A G C C C G G A A A G T T T T T T
 SEQ. ID. NO. 21 A T C C T T G G C C A G T T T G A C C A G A A T A

SEQ. ID. NO. 18 T T C A A A A T T C C A C G G C C A A A G T C A T
 SEQ. ID. NO. 19 T G T G G A A C C T C A T T G T G C T T T C C T A
 SEQ. ID. NO. 20 G T G A G G T G T A C A A G G A G C G T C T C T T
 SEQ. ID. NO. 21 T G G C A G C A A A A G T G T T C T G T T G T G C

Figure 5d

SEQ. ID. NO. 18 C G T G G T T T T C T C C A G T G G C C C A G A T
 SEQ. ID. NO. 19 T G G C T C C A G C T C A C C A G C C C T G T C A
 SEQ. ID. NO. 20 T G G G A A G A A G T A C G T C T G G T T C C T C
 SEQ. ID. NO. 21 A T A C G A G G A G A A C A T G T A T G G T A G T

SEQ. ID. NO. 18 C T T G A G C C C C T C A T C A A G G A G A T T G
 SEQ. ID. NO. 19 A A C C G G C A G C G T T T C C C C A C T T T C T
 SEQ. ID. NO. 20 A T T G G G T G G T A T G C T G A C A A T T G G T
 SEQ. ID. NO. 21 A A A T A T C A G T G G A T C A T T C C G G G C T

SEQ. ID. NO. 18 T C C G G C G C A A T A T C A C G G G C A A G A T
 SEQ. ID. NO. 19 T C C G A A C G C A C C C A T C A G C C A C A C T
 SEQ. ID. NO. 20 T C A A G A T C T A C G A C C C T T C T A T C A A
 SEQ. ID. NO. 21 G G T A C G A G C C T T C T T G G T G G G A G C A

SEQ. ID. NO. 18 C T G G C T G G C C A G C G A G G C C T G G G C C
 SEQ. ID. NO. 19 C C A C A A C C C T A C C C G C G T G A A A C T C
 SEQ. ID. NO. 20 C T G C A C A G T G G A T G A G A T G A C T G A G
 SEQ. ID. NO. 21 G G T G C A C A C G G A A G C C A A C T C A T C C

SEQ. ID. NO. 18 A G C T C C T C C C T G A T C G C C A T G C C T C
 SEQ. ID. NO. 19 T T T G A A A A G T G G G G C T G G A A G A A G A
 SEQ. ID. NO. 20 G C G G T G G A G G G C C A C A T C A C A A C T G
 SEQ. ID. NO. 21 C G C T G C C T C C G G A A G A A T C T G C T T G

SEQ. ID. NO. 18 A G T A C T T C C A C G T G G T T G G C G G C A C
 SEQ. ID. NO. 19 T T G C T A C C A T C C A G C A G A C C A C T G A
 SEQ. ID. NO. 20 A G A T T G T C A T G C T G A A T C C T G C C A A
 SEQ. ID. NO. 21 C T G C C A T G G A G G G C T A C A T T G G C G T

SEQ. ID. NO. 18 C A T T G G A T T C G C T C T G A A G G C T G G G
 SEQ. ID. NO. 19 G G T C T T C A C T T C G A C T C T G G A C G A C
 SEQ. ID. NO. 20 T A C C C G C A G C A T T T C C A A C A T G A C A
 SEQ. ID. NO. 21 G G A T T T C G A G C C C C T G A G C T C C A A G

SEQ. ID. NO. 18 C A G A T C C C A G G C T T C C G G G A A T T C C
 SEQ. ID. NO. 19 C T G G A G G A A C G A G T G A A G G A G G C T G
 SEQ. ID. NO. 20 T C C C A G G A A T T T G T G G A G A A A C T A A
 SEQ. ID. NO. 21 C A G A T C A A G A C C A T C T C A G G A A A G A

Figure 5e

SEQ. ID. NO. 18 T G A A G A A G G T C C A T C C C A G G A A G T C
 SEQ. ID. NO. 19 G A A T T G A G A T T A C T T T C C G C C A G A G
 SEQ. ID. NO. 20 C C A A G C G A C T G A A A A G A C A C C C T G A
 SEQ. ID. NO. 21 C T C C A C A G C A G T A T G A G A G A G A G T A

SEQ. ID. NO. 18 T G T C C A C A A T G G T T T T G C C A A G G A G
 SEQ. ID. NO. 19 T T T C T T C T C A G A T C C A G C T G T G C C C
 SEQ. ID. NO. 20 G G A G A C A G G A G G C T T C C A G G A G G C A
 SEQ. ID. NO. 21 C A A C A A C A A G C G G T C A G G C G T G G G G

SEQ. ID. NO. 18 T T T T G G G A A G A A A C A T T T A A C T G C C
 SEQ. ID. NO. 19 G T C A A A A A C C T G A A G C G C C A G G A T G
 SEQ. ID. NO. 20 C C G C T G G C C T A T G A T G C C A T C T G G G
 SEQ. ID. NO. 21 C C C A G C A A G T T C C A C G G G T A C G C C T

SEQ. ID. NO. 18 A C C T C C A A G A A G G T G C A A A A G G A C C
 SEQ. ID. NO. 19 C C C G A A T C A T C G T G G G A C T T T T C T A
 SEQ. ID. NO. 20 C C T T G G C A C T G G C C C T G A A C A A G A C
 SEQ. ID. NO. 21 A C G A T G G C A T C T G G G T C A T C G C C A A

SEQ. ID. NO. 18 T T T A C C T G T G G A C A C C T T T C T G A G A
 SEQ. ID. NO. 19 T G A G A C T G A A G C C C G G A A A G T T T T T
 SEQ. ID. NO. 20 A T C T G G A G G A G G C G G C C G T T C T G G T
 SEQ. ID. NO. 21 G A C A C T G C A G A G G G C C A T G G A G A C A

SEQ. ID. NO. 18 G G T C A C G A A G A A A G T G G C G A C A G G T
 SEQ. ID. NO. 19 T G T G A G G T G T A C A A G G A G C G T C T C T
 SEQ. ID. NO. 20 G T G C G C C T G G A G G A C T T C A A C T A C A
 SEQ. ID. NO. 21 C T G C A T G C C A G C A G C C G G C A C C A G C

SEQ. ID. NO. 18 T T A G C A A C A G C T C G A C A G C C T T C C G
 SEQ. ID. NO. 19 T T G G G A A G A A G T A C G T C T G G T T C C T
 SEQ. ID. NO. 20 A C A A C C A G A C C A T T A C C G A C C A A A T
 SEQ. ID. NO. 21 G G A T C C A G G A C T T C A A C T A C A C G G A

SEQ. ID. NO. 18 A C C C C T C T G T A C A G G G G A T G A G A A C
 SEQ. ID. NO. 19 C A T T G G G T G G T A T G C T G A C A A T T G G
 SEQ. ID. NO. 20 C T A C C G G G C A A T G A A C T C T T C G T C C
 SEQ. ID. NO. 21 C C A C A C G C T G G G C A G G A T C A T C C T C

Figure 5f

SEQ. ID. NO. 18 A T C A G C A G T G T C G A G A C C C C T T A C A
 SEQ. ID. NO. 19 T T C A A G A T C T A C G A C C C T T C T A T C A
 SEQ. ID. NO. 20 T T T G A G G G T G T C T C T G G C C A T G T G G
 SEQ. ID. NO. 21 A A T G C C A T G A A C G A G A C C A A C T T C T

SEQ. ID. NO. 18 T A G A T T A C A C G C A T T T A C G G A T A T C
 SEQ. ID. NO. 19 A C T G C A C A G T G G A T G A G A T G A C T G A
 SEQ. ID. NO. 20 T G T T T G A T G C C A G C G G C T C T C G G A T
 SEQ. ID. NO. 21 T C G G G G T C A C G G G T C A A G T T G T A T T

SEQ. ID. NO. 18 C T A C A A T G T G T A C T T A G C A G T C T A C
 SEQ. ID. NO. 19 G G C G G T G G A G G G C C A C A T C A C A A C T
 SEQ. ID. NO. 20 G G C A T G G A C G C T T A T C G A G C A G C T T
 SEQ. ID. NO. 21 C C G G A A T G G G G A G A G A A T G G G G A C C

SEQ. ID. NO. 18 T C C A T T G C C C A C G C C T T G C A A G A T A
 SEQ. ID. NO. 19 G A G A T T G T C A T G C T G A A T C C T G C C A
 SEQ. ID. NO. 20 C A G G G T G G C A G C T A C A A G A A G A T T G
 SEQ. ID. NO. 21 A T T A A A T T T A C T C A A T T T C A A G A C A

SEQ. ID. NO. 18 T A T A T A C C T G C T T A C C T G G G A G A G G
 SEQ. ID. NO. 19 A T A C C C G C A G C A T T T C C A A C A T G A C
 SEQ. ID. NO. 20 G C T A C T A T G A C A G C A C C A A G G A T G A
 SEQ. ID. NO. 21 G C A G G G A G G T G A A G G T G G G A G A G T A

SEQ. ID. NO. 18 G C T C T T C A C C A A T G G C T C C T G T G C A
 SEQ. ID. NO. 19 A T C C C A G G A A T T T G T G G A G A A A C T A
 SEQ. ID. NO. 20 T C T T T C C T G G T C C A A A A C A G A T A A A
 SEQ. ID. NO. 21 C A A C G C T G T G G C C G A C A C A C T G G A G

SEQ. ID. NO. 18 G A C A T C A A G A A A G T T G A G G C G T G G C
 SEQ. ID. NO. 19 A C C A A G C G A C T G A A A A G A C A C C C T G
 SEQ. ID. NO. 20 T G G A T T G G A G G G T C C C C C C C A G C T G
 SEQ. ID. NO. 21 A T C A T C A A T G A C A C C A T C A G G T T C C

SEQ. ID. NO. 18 A G G T C C T G A A G C A C C T A C G G C A T C T
 SEQ. ID. NO. 19 A G G A G A C A G G A G G C T T C C A G G A G G C
 SEQ. ID. NO. 20 A C C A G A C C C T G G T C A T C A A G A C A T T
 SEQ. ID. NO. 21 A A G G A T C C G A A C C A C C A A A A G A C A A

Figure 5g

SEQ. ID. NO. 18 A A A C T T T A C A A A C A A T A T G G G G G A G
 SEQ. ID. NO. 19 A C C G C T G G C C T A T G A T G C C A T C T G G
 SEQ. ID. NO. 20 C C G C T T C C T G T C A C A G A A A C T C T T T
 SEQ. ID. NO. 21 G A C C A T C A T C C T G G A G C A G C T G C G G

SEQ. ID. NO. 18 C A G G T G A C C T T T G A T G A G T G T G G T G
 SEQ. ID. NO. 19 G C C T T G G C A C T G G C C C T G A A C A A G A
 SEQ. ID. NO. 20 A T C T C C G T C T C A G T T C T C T C C A G C C
 SEQ. ID. NO. 21 A A G A T C T C C C T A C C T C T C T A C A G C A

SEQ. ID. NO. 18 A C C T G G T G G G G A A C T A T T C C A T C A T
 SEQ. ID. NO. 19 C A T C T G G A G G A G G C G G C C G T T C T G G
 SEQ. ID. NO. 20 T G G G C A T T G T C C T A G C T G T T G T C T G
 SEQ. ID. NO. 21 T C C T C T C T G C C C T C A C C A T C C T C G G

SEQ. ID. NO. 18 C A A C T G G C A C C T C T C C C C A G A G G A T
 SEQ. ID. NO. 19 T G T G C G C C T G G A G G A C T T C A A C T A C
 SEQ. ID. NO. 20 T C T G T C C T T T A A C A T C T A C A A C T C A
 SEQ. ID. NO. 21 G A T G A T C A T G G C C A G T G C T T T T C T C

SEQ. ID. NO. 18 G G C T C C A T C G T G T T T A A G G A A G T C G
 SEQ. ID. NO. 19 A A C A A C C A G A C C A T T A C C G A C C A A A
 SEQ. ID. NO. 20 C A T G T C C G T T A T A T C C A G A A C T C A C
 SEQ. ID. NO. 21 T T C T T C A A C A T C A A G A A C C G G A A T C

SEQ. ID. NO. 18 G G T A T T A C A A C G T C T A T G C C A A G A A
 SEQ. ID. NO. 19 T C T A C C G G G C A A T G A A C T C T T C G T C
 SEQ. ID. NO. 20 A G C C C A A C C T G A A C A A C C T G A C T G C
 SEQ. ID. NO. 21 A G A A G C T C A T A A A G A T G T C G A G T C C

SEQ. ID. NO. 18 G G G A G A A A G A C T C T T C A T C A A C G A G
 SEQ. ID. NO. 19 C T T T G A G G G T G T C T C T G G C C A T G T G
 SEQ. ID. NO. 20 T G T G G G C T G C T C A C T G G C T T T A G C T
 SEQ. ID. NO. 21 A T A C A T G A A C A A C C T T A T C A T C C T T

SEQ. ID. NO. 18 G A G A A A A T C C T G T G G A G T G G G T T C T
 SEQ. ID. NO. 19 G T G T T T G A T G C C A G C G G C T C T C G G A
 SEQ. ID. NO. 20 G C T G T C T T C C C C C T G G G G C T C G A T G
 SEQ. ID. NO. 21 G G A G G G A T G C T C T C C T A T G C T T C C A

Figure 5h

SEQ. ID. NO. 18 C C A G G G A G G T G C C C T T C T C C A A C T G
 SEQ. ID. NO. 19 T G G C A T G G A C G C T T A T C G A G C A G C T
 SEQ. ID. NO. 20 G T T A C C A C A T T G G G A G G A A C C A G T T
 SEQ. ID. NO. 21 T A T T T C T C T T T G G C C T T G A T G G A T C

SEQ. ID. NO. 18 C A G C C G A G A C T G C C T G G C A G G G A C C
 SEQ. ID. NO. 19 T C A G G G T G G C A G C T A C A A G A A G A T T
 SEQ. ID. NO. 20 T C C T T T C G T C T G C C A G G C C C G C C T C
 SEQ. ID. NO. 21 C T T T G T C T C T G A A A A G A C C T T T G A A

SEQ. ID. NO. 18 A G G A A A G G G A T C A T T G A G G G G G A G C
 SEQ. ID. NO. 19 G G C T A C T A T G A C A G C A C C A A G G A T G
 SEQ. ID. NO. 20 T G G C T C C T G G G C C T G G G C T T T A G T C
 SEQ. ID. NO. 21 A C A C T T T G C A C C G T C A G G A C C T G G A

SEQ. ID. NO. 18 C C A C C T G C T G C T T T G A G T G T G T G G A
 SEQ. ID. NO. 19 A T C T T T C C T G G T C C A A A A C A G A T A A
 SEQ. ID. NO. 20 T G G G C T A C G G T T C C A T G T T C A C C A A
 SEQ. ID. NO. 21 T T C T C A C C G T G G G C T A C A C G A C C G C

SEQ. ID. NO. 18 G T G T C C T G A T G G G G A G T A T A G T G A T
 SEQ. ID. NO. 19 A T G G A T T G G A G G G T C C C C C C C A G C T
 SEQ. ID. NO. 20 G A T T T G G T G G G T C C A C A C G G T C T T C
 SEQ. ID. NO. 21 T T T T G G G G C C A T G T T T G C A A A G A C C

SEQ. ID. NO. 18 G A G A C A G A T G C C A G T G C C T G T A A C A
 SEQ. ID. NO. 19 G A C C A G A C C C T G G T C A T C A A G A C A T
 SEQ. ID. NO. 20 A C A A A G A A G G A A G A A A A G A A G G A G T
 SEQ. ID. NO. 21 T G G A G A G T C C A C G C C A T C T T C A A A A

SEQ. ID. NO. 18 A G T G C C C A G A T G A C T T C T G G T C C A A
 SEQ. ID. NO. 19 T C C G C T T C C T G T C A C A G A A A C T C T T
 SEQ. ID. NO. 20 G G A G G A A G A C T C T G G A A C C C T G G A A
 SEQ. ID. NO. 21 A T G T G A A A A T G A A G A A G A A G A T C A T

SEQ. ID. NO. 18 T G A G A A C C A C A C C T C C T G C A T T G C C
 SEQ. ID. NO. 19 T A T C T C C G T C T C A G T T C T C T C C A G C
 SEQ. ID. NO. 20 G C T G T A T G C C A C A G T G G G C C T G C T G
 SEQ. ID. NO. 21 C A A G G A C C A G A A A C T G C T T G T G A T C

Figure 5i

SEQ. ID. NO. 18 A A G G A G A T C G A G T T T C T G T C G T G G A
 SEQ. ID. NO. 19 C T G G G C A T T G T C C T A G C T G T T G T C T
 SEQ. ID. NO. 20 G T G G G C A T G G A T G T C C T C A C T C T C G
 SEQ. ID. NO. 21 G T G G G G G G C A T G C T G C T G A T C G A C C

SEQ. ID. NO. 18 C G G A G C C C T T T G G G A T C G C A C T C A C
 SEQ. ID. NO. 19 G T C T G T C C T T T A A C A T C T A C A A C T C
 SEQ. ID. NO. 20 C C A T C T G G C A G A T C G T G G A C C C T C T
 SEQ. ID. NO. 21 T G T G T A T C C T G A T C T G C T G G C A G G C

SEQ. ID. NO. 18 C C T C T T T G C C G T G C T G G G C A T T T T C
 SEQ. ID. NO. 19 A C A T G T C C G T T A T A T C C A G A A C T C A
 SEQ. ID. NO. 20 G C A C C G G A C C A T T G A G A C A T T T G C C
 SEQ. ID. NO. 21 T G T G G A C C C C C T G C G A A G G A C A G T G

SEQ. ID. NO. 18 C T G A C A G C C T T T G T G C T G G G T G T G T
 SEQ. ID. NO. 19 C A G C C C A A C C T G A A C A A C C T G A C T G
 SEQ. ID. NO. 20 A A G G A G G A A C C T A A G G A A G A T A T T G
 SEQ. ID. NO. 21 G A G A A G T A C A G C A T G G A G C C G G A C C

SEQ. ID. NO. 18 T T A T C A A G T T C C G C A A C A C A C C C A T
 SEQ. ID. NO. 19 C T G T G G G C T G C T C A C T G G C T T T A G C
 SEQ. ID. NO. 20 A C G T C T C T A T T C T G C C C C A G C T G G A
 SEQ. ID. NO. 21 C A G C A G G A C G G G A T A T C T C C A T C C G

SEQ. ID. NO. 18 T G T C A A G G C C A C C A A C C G A G A G C T C
 SEQ. ID. NO. 19 T G C T G T C T T C C C C C T G G G G C T C G A T
 SEQ. ID. NO. 20 G C A T T G C A G C T C C A G G A A G A T G A A T
 SEQ. ID. NO. 21 C C C T C T C C T G G A G C A C T G T G A G A A C

SEQ. ID. NO. 18 T C C T A C C T C C T C C T C T T C T C C C T G C
 SEQ. ID. NO. 19 G G T T A C C A C A T T G G G A G G A A C C A G T
 SEQ. ID. NO. 20 A C A T G G C T T G G C A T T T T C T A T G G T T
 SEQ. ID. NO. 21 A C C C A T A T G A C C A T C T G G C T T G G C A

SEQ. ID. NO. 18 T C T G C T G C T T C T C C A G C T C C C T G T T
 SEQ. ID. NO. 19 T T C C T T T C G T C T G C C A G G C C C G C C T
 SEQ. ID. NO. 20 A C A A G G G G C T G C T G C T G C T G G G
 SEQ. ID. NO. 21 T C G T C T A T G C C T A C A A G G G A C T T C T

Figure 5J

SEQ. ID. NO. 18 C T T C A T C G G G G A G C C C C A G G A C T G G
 SEQ. ID. NO. 19 C T G G C T C C T G G G C C T G G G C T T T A G T
 SEQ. ID. NO. 20 A A T C T T C C T T G C T T A T G A G A C C A A G
 SEQ. ID. NO. 21 C A T G T T G T T C G G T T G T T T C T T A G C T

SEQ. ID. NO. 18 A C G T G C C G C C T G C G C C A G C C G G C C T
 SEQ. ID. NO. 19 C T G G G C T A C G G T T C C A T G T T C A C C A
 SEQ. ID. NO. 20 A G T G T G T C C A C T G A G A A G A T C A A T G
 SEQ. ID. NO. 21 T G G G A G A C C C G C A A C G T C A G C A T C C

SEQ. ID. NO. 18 T T G G C A T C A G C T T C G T G C T C T G C A T
 SEQ. ID. NO. 19 A G A T T T G G T G G G T C C A C A C G G T C T T
 SEQ. ID. NO. 20 A T C A C C G G G C T G T G G G C A T G G C T A T
 SEQ. ID. NO. 21 C C G C A C T C A A C G A C A G C A A G T A C A T

SEQ. ID. NO. 18 C T C A T G C A T C C T G G T G A A A A C C A A C
 SEQ. ID. NO. 19 C A C A A A G A A G G A A G A A A A G A A G G A G
 SEQ. ID. NO. 20 C T A C A A T G T G G C A G T C C T G T G C C T C
 SEQ. ID. NO. 21 C G G G A T G A G T G T C T A C A A C G T G G G G

SEQ. ID. NO. 18 C G T G T C C T C C T G G T G T T T G A G G C C A
 SEQ. ID. NO. 19 T G G A G G A A G A C T C T G G A A C C C T G G A
 SEQ. ID. NO. 20 A T C A C T G C T C C T G T C A C C A T G A T T C
 SEQ. ID. NO. 21 A T C A T G T G C A T C A T C G G G G C C G C T G

SEQ. ID. NO. 18 A G A T C C C C A C C A G C T T C C A C C G C A A
 SEQ. ID. NO. 19 A G C T G T A T G C C A C A G T G G G C C T G C T
 SEQ. ID. NO. 20 T G T C C A G C C A G C A G G A T G C A G C C T T
 SEQ. ID. NO. 21 T C T C C T T C C T G A C C C G G G A C C A G C C

SEQ. ID. NO. 18 G T G G T G G G G G C T C A A C C T G C A G T T C
 SEQ. ID. NO. 19 G G T G G G C A T G G A T G T C C T C A C T C T C
 SEQ. ID. NO. 20 T G C C T T T G C C T C T C T T G C C A T A G T T
 SEQ. ID. NO. 21 C A A T G T G C A G T T C T G C A T C G T G G C T

SEQ. ID. NO. 18 C T G C T G G T T T T C C T C T G C A C C T T C A
 SEQ. ID. NO. 19 G C C A T C T G G C A G A T C G T G G A C C C T C
 SEQ. ID. NO. 20 T T C T C C T C C T A T A T C A C T C T T G T T G
 SEQ. ID. NO. 21 C T G G T C A T C A T C T T C T G C A G C A C C A

Figure 5k

SEQ. ID. NO. 18 T G C A G A T T G T C A T C T G T G T G A T C T G
 SEQ. ID. NO. 19 T G C A C C G G A C C A T T G A G A C A T T T G C
 SEQ. ID. NO. 20 T G C T C T T T G T G C C C A A G A T G C G C A G
 SEQ. ID. NO. 21 T C A C C C T C T G C C T G G T A T T C G T G C C

SEQ. ID. NO. 18 G C T C T A C A C C G C G C C C C C C T C A A G C
 SEQ. ID. NO. 19 C A A G G A G G A A C C T A A G G A A G A T A T T
 SEQ. ID. NO. 20 G C T G A T C A C C C G A G G G G A A T G G C A G
 SEQ. ID. NO. 21 G A A G C T C A T C A C C C T G A G A A C A A A C

SEQ. ID. NO. 18 T A C C G C A A C C A G G A G C T G G A G G A T G
 SEQ. ID. NO. 19 G A C G T C T C T A T T C T G C C C C A G C T G G
 SEQ. ID. NO. 20 T C G G A G G C G C A G G A C A C C A T G A A G A
 SEQ. ID. NO. 21 C C A G A T G C A G C A A C G C A G A A C A G G C

SEQ. ID. NO. 18 A G A T C A T C T T C A T C A C G T G C C A C G A
 SEQ. ID. NO. 19 A G C A T T G C A G C T C C A G G A A G A T G A A
 SEQ. ID. NO. 20 C A G G G T C A T C G A C C A A C A A C A A C G A
 SEQ. ID. NO. 21 G A T T C C A G T T C A C T C A G A A T C A G A A

SEQ. ID. NO. 18 G G G C T C C C T C A T G G C C C T G G G C T T C
 SEQ. ID. NO. 19 T A C A T G G C T T G G C A T T T T C T A T G G T
 SEQ. ID. NO. 20 G G A G G A G A A G T C C C G G C T G T T G G A G
 SEQ. ID. NO. 21 G A A A G A A G A T T C T A A A A C G T C C A C C

SEQ. ID. NO. 18 C T G A T C G G C T A C A C C T G C C T G C T G G
 SEQ. ID. NO. 19 T A C A A G G G G C T G C T G C T G C T G C T G G
 SEQ. ID. NO. 20 A A G G A G A A C C G T G A A C T G G A A A A G A
 SEQ. ID. NO. 21 T C G G T C A C C A G T G T G A A C C A A G C C A

SEQ. ID. NO. 18 C T G C C A T C T G C T T C T T C T T T G C C T T
 SEQ. ID. NO. 19 G A A T C T T C C T T G C T T A T G A G A C C A A
 SEQ. ID. NO. 20 T C A T T G C T G A G A A A G A G G A G C G T G T
 SEQ. ID. NO. 21 G C A C A T C C C G C C T G G A G G G C C T A C A

SEQ. ID. NO. 18 C A A G T C C C G G A A G C T G C C G G A G A A C
 SEQ. ID. NO. 19 G A G T G T G T C C A C T G A G A A G A T C A A T
 SEQ. ID. NO. 20 C T C T G A A C T G C G C C A T C A A C T C C A G
 SEQ. ID. NO. 21 G T C A G A A A A C C A T C G C C T G C G A A T G

Figure 51

SEQ. ID. NO. 18 T T C A A T G A A G C C A A G T T C A T C A C C T
 SEQ. ID. NO. 19 G A T C A C C G G G C T G T G G G C A T G G C T A
 SEQ. ID. NO. 20 T C T C G G C A G C A G C T C C G C T C C C G G C
 SEQ. ID. NO. 21 A A G A T C A C A G A G C T G G A T A A A G A C T

SEQ. ID. NO. 18 T C A G C A T G C T C A T C T T C T T C A T C G T
 SEQ. ID. NO. 19 T C T A C A A T G T G G C A G T C C T G T G C C T
 SEQ. ID. NO. 20 G C C A C C C A C C G A C A C C C C C A G A A C C
 SEQ. ID. NO. 21 T G G A A G A G G T C A C C A T G C A G C T G C A

SEQ. ID. NO. 18 C T G G A T C T C C T T C A T T C C A G C C T A T
 SEQ. ID. NO. 19 C A T C A C T G C T C C T G T C A C C A T G A T T
 SEQ. ID. NO. 20 C T C T G G G G G C C T G C C C A G G G G A C C C
 SEQ. ID. NO. 21 G G A C A C A C C A G A A A A G A C C A C C T A C

SEQ. ID. NO. 18 G C C A G C A C C T A T G G C A A G T T T G T C T
 SEQ. ID. NO. 19 C T G T C C A G C C A G C A G G A T G C A G C C T
 SEQ. ID. NO. 20 C C T G A G C C C C C C G A C C G G C T T A G C T
 SEQ. ID. NO. 21 A T T A A A C A G A A C C A C T A C C A A G A G C

SEQ. ID. NO. 18 C T G C C G T A G A G G T G A T T G C C A T C C T
 SEQ. ID. NO. 19 T T G C C T T T G C C T C T C T T G C C A T A G T
 SEQ. ID. NO. 20 G T G A T G G G A G T C G A G T G C A T T T G C T
 SEQ. ID. NO. 21 T C A A T G A C A T C C T C A A C C T G G G A A A

SEQ. ID. NO. 18 G G C A G C C A G C T T T G G C T T G C T G G C G
 SEQ. ID. NO. 19 T T T C T C C T C C T A T A T C A C T C T T G T T
 SEQ. ID. NO. 20 T T A T A A G T G A G G G T A G G G T G A G G G A
 SEQ. ID. NO. 21 C T T C A C T G A G A G C A C A G A T G G A G G A

SEQ. ID. NO. 18 T G C A T C T T C T T C A A C A A G A T C T A C A
 SEQ. ID. NO. 19 G T G C T C T T T G T G C C C A A G A T G C G C A
 SEQ. ID. NO. 20 G G A C A G G C C A G T A G G G G G A G G G A A A
 SEQ. ID. NO. 21 A A G G C C A T T T T A A A A A A T C A C C T C G

SEQ. ID. NO. 18 T C A T T C T C T T C A A G C C A T C C C G C A A
 SEQ. ID. NO. 19 G G C T G A T C A C C C G A G G G G A A T G G C A
 SEQ. ID. NO. 20 G G G A G A G G G G A A G G G C A G G G G A C T C
 SEQ. ID. NO. 21 A T C A A A A T C C C C A G C T A C A G T G G A A

Figure 5m

SEQ. ID. NO. 18 C A C C A T C G A G G A G G T G C G T T G C A G C
 SEQ. ID. NO. 19 G T C G G A G G C G C A G G A C A C C A T G A A G
 SEQ. ID. NO. 20 A G G A A G C A G G G G G T C C C C A T C C C C A
 SEQ. ID. NO. 21 C A C A A C A G A G C C C T C T C G A A C A T G C

SEQ. ID. NO. 18 A C C G C A G C T C A C G C T T T C A A G G T G G
 SEQ. ID. NO. 19 A C A G G G T C A T C G A C C A A C A A C A A C G
 SEQ. ID. NO. 20 G C T G G G A A G A A C A T G C T A T C C A A T C
 SEQ. ID. NO. 21 A A A G A T C C T A T A G A A G A T A T A A A C T

SEQ. ID. NO. 18 C T G C C C G G G C C A C G C T G C G C C G C A G
 SEQ. ID. NO. 19 A G G A G G A G A A G T C C C G G C T G T T G G A
 SEQ. ID. NO. 20 T C A T C T C T T G T A A A T A C A T G T C C C C
 SEQ. ID. NO. 21 C T C C A G A A C A C A T C C A G C G T C G G C T

SEQ. ID. NO. 18 C A A C G T C T C C C G C A A G C G G T C C A G C
 SEQ. ID. NO. 19 G A A G G A G A A C C G T G A A C T G G A A A A G
 SEQ. ID. NO. 20 C T G T G A G T T C T G G G C T G A T T T G G G T
 SEQ. ID. NO. 21 G T C C C T C C A G C T C C C C A T C C T C C A C

SEQ. ID. NO. 18 A G C C T T G G A G G C T C C A C G G G A T C C A
 SEQ. ID. NO. 19 A T C A T T G C T G A G A A A G A G G A G C G T G
 SEQ. ID. NO. 20 C T C T C A T A C C T C T G G G A A A C A G A C C
 SEQ. ID. NO. 21 C A C G C C T A C C T C C C A T C C A T C G G A G

SEQ. ID. NO. 18 C C C C C T C C T C C T C C A T C A G C A G C A A
 SEQ. ID. NO. 19 T C T C T G A A C T G C G C C A T C A G C T C C A
 SEQ. ID. NO. 20 T T T T T C T C T C T T A C T G C T T C A T G T A
 SEQ. ID. NO. 21 G C G T G G A C G C C A G C T G T G T C A G C C C

SEQ. ID. NO. 18 G A G C A A C A G C G A A G A C C C A T T C C C A
 SEQ. ID. NO. 19 G T C T C G G C A G C A G C T C C G C T C C C G G
 SEQ. ID. NO. 20 A T T T T G T A T C A C C T C T T C A C A A T T T
 SEQ. ID. NO. 21 C T G C G T C A G C C C C A C C G C C A G C C C C

SEQ. ID. NO. 18 C A G C C C G A G A G G C A G A A G C A G C A G C
 SEQ. ID. NO. 19 C G C C A C C C A C C G A C A C C C C C A G A A C
 SEQ. ID. NO. 20 A G T T C G T A C C T G G C T T G A A G C T G C T
 SEQ. ID. NO. 21 C G C C A C A G A C A T G T G C C A C C C T C C T

Figure 5n

SEQ. ID. NO. 18 A G C C G C T G G C C C T A A C C C A G C A A G A
 SEQ. ID. NO. 19 C C T C T G G G G G C C T G C C C A G G G G A C C
 SEQ. ID. NO. 20 C A C T G C T C A C A C G C T G C C T C C T C A G
 SEQ. ID. NO. 21 T C C G A G T C A T G G T C T C G G G C C T G T A

SEQ. ID. NO. 18 G C A G C A G C A G C A G C C C C T G A C C C T C
 SEQ. ID. NO. 19 C C C T G A G C C C C C G A C C G G C T T A G C
 SEQ. ID. NO. 20 C A G C C T C A C T G C A T C T T T C T C T T C C
 SEQ. ID. NO. 21 A G G G T G G G A G G C C T G G G C C C G G G G C

SEQ. ID. NO. 18 C C A C A G C A G C A A C G A T C T C A G C A G C
 SEQ. ID. NO. 19 T G T G A T G G G A G T C G A G T G C A T T T G C
 SEQ. ID. NO. 20 C A T G C A A C A C C C T C T T C T A G T T A C C
 SEQ. ID. NO. 21 C T C C C C C G T G A C A G A A C C A C A C T G G

SEQ. ID. NO. 18 A G C C C A G A T G C A A G C A G A A G G T C A T
 SEQ. ID. NO. 19 T T T A T A A G T G A G G G T A G G G T G A G G G
 SEQ. ID. NO. 20 A C G G C A A C C C C T
 SEQ. ID. NO. 21 G C A G A G G G G T C T G C T G C A G A A A C A C

SEQ. ID. NO. 18 C T T T G G C A G C G G C A C G G T C A C C T T C
 SEQ. ID. NO. 19 A G G A C A G G C C A G T A G G G G G A G G G A A
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 T G T C G G C T C T G G C T G C G G A G A A G C T

SEQ. ID. NO. 18 T C A C T G A G C T T T G A T G A G C C T C A G A
 SEQ. ID. NO. 19 A G G G A G A G G G G A A G G G C A G G G G A C T
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 G G G C A C C A T G G C T G G C C T C T C A G G A

SEQ. ID. NO. 18 A G A A C G C C A T G G C C C A C G G G A A T T C
 SEQ. ID. NO. 19 C A G G A A G C A G G G G G T C C C C A T C C C C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 C C A C T C G G A T G G C A C T C A G G T G G A C

SEQ. ID. NO. 18 T A C G C A C C A G A A C T C C C T G G A G G C C
 SEQ. ID. NO. 19 A G C T G G G A A G A A C A T G C T A T C C A A T
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A G G A C G G G G C A G G G G G A G A C T T G G C

Figure 5o

SEQ. ID. NO. 18 C A G A A A A G C A G C G A T A C G C T G A C C C
 SEQ. ID. NO. 19 C T C A T C T C T T G T A A A T A C A T G T C C C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A C C T G A C C T C G A G C C T T A T T T G T G A

SEQ. ID. NO. 18 G A C A C C A G C C A T T A C T C C C G C T G C A
 SEQ. ID. NO. 19 C C T G T G A G T T C T G G G C T G A T T T G G G
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A G T C C T T A T T T C T T C A C A A A G A A G A

SEQ. ID. NO. 18 G T G C G G G G A A A C G G A C T T A G A T C T G
 SEQ. ID. NO. 19 T C T C T C A T A C C T C T G G G A A A C A G A C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 G G A A C G G A A A T G G G A C G T C T T C C T T

SEQ. ID. NO. 18 A C C G T C C A G G A A A C A G G T C T G C A A G
 SEQ. ID. NO. 19 C T T T T T C T C T C T T A C T G C T T C A T G T
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A A C A T C T G C A A A C A A G G A G G C G C T G

SEQ. ID. NO. 18 G A C C T G T G G G T G G A G A C C A G C G G C C
 SEQ. ID. NO. 19 A A T T T T G T A T C A C C T C T T C A C A A T T
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 G G A T A T C A A A C T T G C A A A A A A A A A A

SEQ. ID. NO. 18 A G A G G T G G A G G A C C C T G A A G A G T T G
 SEQ. ID. NO. 19 T A G T T C G T A C C T G G C T T G A A G C T G C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A A A A A A A A A A A A A A

SEQ. ID. NO. 18 T C C C C A G C A C T T G T A G T G T C C A G T T
 SEQ. ID. NO. 19 T C A C T G C T C A C A C G C T G C C T C C T C A
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21

SEQ. ID. NO. 18 C A C A G A G C T T T G T C A T C A G T G G T G G
 SEQ. ID. NO. 19 G C A G C C T C A C T G C A T C T T T C T C T T C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21

Figure 5p

SEQ. ID. NO. 18 A G G C A G C A C T G T T A C A G A A A C G T A
SEQ. ID. NO. 19 C C A T G C A A C A C C C T C T T C T A G T T A C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18 G T G A A T T C A
SEQ. ID. NO. 19 C A C G G C A A C C C C T G C A G C T C C T C T G
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C T T T G T G C T C T G T T C C T G T C C A G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 A G G G G T C T C C C A A C A A G T G C T C T T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C A C C C C A A A G G G G C C T C T C C T T T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C T C C A C T G T C A T A A T C T C T T T C C A T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C T T A C T T G C C C T T C T A T A C T T T C T C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 A C A T G T G G C T C C C C C T G A A T T T T G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

Figure 5q

SEQ. ID. NO. 18

SEQ. ID. NO. 19 T T C C T T T G G G G A G C T C A T T C T T T C G

SEQ. ID. NO. 20

SEQ. ID. NO. 21

SEQ. ID. NO. 18

SEQ. ID. NO. 19 C C A A G G T C A C A T G C T C C C T T G C C T C

SEQ. ID. NO. 20

SEQ. ID. NO. 21

SEQ. ID. NO. 18

SEQ. ID. NO. 19 T G G C T C C G T G C A

SEQ. ID. NO. 20

SEQ. ID. NO. 21

Figure 5r

FIGURE 6a

SEQ. ID. NO. 22 A T G C T G C T G C T G C T G C T G G T G C C T C T C T T C
SEQ. ID. NO. 23 A T G G G C C C G G G G G G A C C C T G T A C C C C A G T G

SEQ. ID. NO. 22 C T C C G C C C C C T G G G C G C T G G C G G G G C G C A G
SEQ. ID. NO. 23 G G G T G G C C G C T G C C T C T T C T G C T G G T G A T G

SEQ. ID. NO. 22 A C C C C C A A C G C C A C C T C G G A A G G T T G C C A G
SEQ. ID. NO. 23 G C G G C T G G G G T G G C T C C G G T G T G G G C C T C T

SEQ. ID. NO. 22 A T T A T A C A T C C G C C C T G G G A A G G T G G C A T C
SEQ. ID. NO. 23 C A C T C C C C T C A T C T C C C G C G G C C T C A C C C G

SEQ. ID. NO. 22 A G G T A C C G T G G C T T G A C T C G C G A C C A G G T G
SEQ. ID. NO. 23 A G G G T C C C C C C G C A C C C C T C C T C A G A A C G G

SEQ. ID. NO. 22 A A G G C C A T C A A C T T C C T G C C T G T G G A C T A T
SEQ. ID. NO. 23 C G T G C A G T A T A C A T C G G G G C G C T G T T T C C C

SEQ. ID. NO. 22 G A G A T C G A A T A T G T G T G C C G A G G G G A G C G C
SEQ. ID. NO. 23 A T G A G C G G G G G C T G G C C G G G G G C C A G G C C

SEQ. ID. NO. 22 G A G G T G G T G G G G C C C A A G G T G C G C A A A T G C
SEQ. ID. NO. 23 T G C C A G C C C G C G G T G G A G A T G G C G C T G G A G

SEQ. ID. NO. 22 C T G G C C A A C G G C T C C T G G A C G G A T A T G G A C
SEQ. ID. NO. 23 G A C G T T A A C A G C C G C A G A G A C A T C C T G C C G

SEQ. ID. NO. 22 A C A C C C A G C C G C T G T G T C C G A A T C T G C T C C
SEQ. ID. NO. 23 G A C T A C G A G C T C A A G C T T A T C C A C C A C G A C

SEQ. ID. NO. 22 A A G T C T T A T T T G A C C C T G G A A A A T G G G A A G
SEQ. ID. NO. 23 A G C A A G T G T G A C C C A G G G C A A G C C A C C A A G

SEQ. ID. NO. 22 G T T T T C C T G A C G G G T G G G G A C C T C C C A G C T
SEQ. ID. NO. 23 T A C T T G T A C G A A C T A C T C T A C A A T G A C C C C

FIGURE 6b

SEQ. ID. NO. 22 C T G G A T G G A G C C C G G G T G G A G T T C C G A T G T
SEQ. ID. NO. 23 A T C A A G A T C A T T C T C A T G C C T G G C T G T A G T

SEQ. ID. NO. 22 G A C C C C G A C T T C C A T C T G G T G G G C A G C T C C
SEQ. ID. NO. 23 T C T G T C T C C A C A C T T G T A G C T G A G G C T G C C

SEQ. ID. NO. 22 C G G A G C G T C T G T A G T C A G G G C C A G T G G A G C
SEQ. ID. NO. 23 C G G A T G T G G A A C C T T A T T G T G C T C T C A T A T

SEQ. ID. NO. 22 A C C C C C A A G C C C C A C T G C C A G G T G A A T C G A
SEQ. ID. NO. 23 G G C T C C A G T T C A C C A G C C T T G T C A A A C C G A

SEQ. ID. NO. 22 A C G C C A C A C T C A G A A C G G C G T G C A G T A T A C
SEQ. ID. NO. 23 C A G C G G T T T C C C A C G T T C T T C C G G A C G C A T

SEQ. ID. NO. 22 A T C G G G G C G C T G T T T C C C A T G A G C G G G G G C
SEQ. ID. NO. 23 C C A T C C G C C A C A C T C C A C A A T C C C A C C C G G

SEQ. ID. NO. 22 T G G C C G G G G G G C C A G G C C T G C C A G C C C G C G
SEQ. ID. NO. 23 G T G A A A C T C T T C G A A A A G T G G G G C T G G A A G

SEQ. ID. NO. 22 G T G G A G A T G G C G C T G G A G G A C G T T A A C A G C
SEQ. ID. NO. 23 A A G A T C G C T A C C A T C C A A C A G A C C A C C G A G

SEQ. ID. NO. 22 C G C A G A G A C A T C C T G C C G G A C T A C G A G C T C
SEQ. ID. NO. 23 G T C T T C A C C T C A A C G C T G G A T G A C C T G G A G

SEQ. ID. NO. 22 A A G C T T A T C C A C C A C G A C A G C A A G T G T G A C
SEQ. ID. NO. 23 G A G C G A G T G A A A G A G G C T G G G A T C G A G A T C

SEQ. ID. NO. 22 C C A G G G C A A G C C A C C A A G T A C T T G T A C G A A
SEQ. ID. NO. 23 A C T T T C C G A C A G A G T T T C T T C T C G G A T C C A

SEQ. ID. NO. 22 C T A C T C T A C A A T G A C C C C A T C A A G A T C A T T
SEQ. ID. NO. 23 G C T G T G C C T G T T A A A A C C T G A A G C G T C A A

SEQ. ID. NO. 22 C T C A T G C C T G G C T G T A G T T C T G T C T C C A C A
SEQ. ID. NO. 23 G A T G C T C G A A T C A T C G T G G G A C T T T T C T A T

FIGURE 6c

SEQ. ID. NO. 22 C T T G T A G C T G A G G C T G C C C G G A T G T G G A A C
SEQ. ID. NO. 23 G A G A C G G A A G C C C G G A A A G T T T T T T G T G A G

SEQ. ID. NO. 22 C T T A T T G T G C T C T C A T A T G G C T C C A G T T C A
SEQ. ID. NO. 23 G T C T A T A A G G A A A G G C T C T T T G G G A A G A A G

SEQ. ID. NO. 22 C C A G C C T T G T C A A A C C G A C A G C G G T T T C C C
SEQ. ID. NO. 23 T A C G T C T G G T T C C T C A T C G G G T G G T A T G C T

SEQ. ID. NO. 22 A C G T T C T T C C G G A C G C A T C C A T C C G C C A C A
SEQ. ID. NO. 23 G A C A A C T G G T T C A A G A C C T A T G A C C C G T C A

SEQ. ID. NO. 22 C T C C A C A A T C C C A C C C G G G T G A A A C T C T T C
SEQ. ID. NO. 23 A T C A A T T G T A C A G T G G A A G A A A T G A C C G A G

SEQ. ID. NO. 22 G A A A A G T G G G G C T G G A A G A A G A T C G C T A C C
SEQ. ID. NO. 23 G C G G T G G A G G G C C A C A T C A C C A C G G A G A T T

SEQ. ID. NO. 22 A T C C A A C A G A C C A C C G A G G T C T T C A C C T C A
SEQ. ID. NO. 23 G T C A T G C T G A A C C C T G C C A A C A C C C G A A G C

SEQ. ID. NO. 22 A C G C T G G A T G A C C T G G A G G A G C G A G T G A A A
SEQ. ID. NO. 23 A T T T C C A A C A T G A C G T C A C A G G A A T T T G T G

SEQ. ID. NO. 22 G A G G C T G G G A T C G A G A T C A C T T T C C G A C A G
SEQ. ID. NO. 23 G A G A A A C T A A C C A A G C G G C T G A A A A G A C A C

SEQ. ID. NO. 22 A G T T T C T T C T C G G A T C C A G C T G T G C C T G T T
SEQ. ID. NO. 23 C C C G A G G A G A C T G G A G G C T T C C A G G A G G C A

SEQ. ID. NO. 22 A A A A A C C T G A A G C G T C A A G A T G C T C G A A T C
SEQ. ID. NO. 23 C C A C T G G C C T A T G A T G C T A T C T G G G C C T T G

SEQ. ID. NO. 22 A T C G T G G G A C T T T T C T A T G A G A C G G A A G C C
SEQ. ID. NO. 23 G C T T T G G C C T T G A A C A A G A C G T C T G G A G G A

SEQ. ID. NO. 22 C G G A A A G T T T T T T G T G A G G T C T A T A A G G A A
SEQ. ID. NO. 23 G G T G G T C G T T C C G G C G T G C G C C T G G A G G A C

FIGURE 6d

SEQ. ID. NO. 22 A G G C T C T T T G G G A A G A A G T A C G T C T G G T T C
SEQ. ID. NO. 23 T T T A A C T A C A A C A A C C A G A C C A T T A C A G A C

SEQ. ID. NO. 22 C T C A T C G G G T G G T A T G C T G A C A A C T G G T T C
SEQ. ID. NO. 23 C A G A T C T A C C G G G C C A T G A A C T C C T C C T C C

SEQ. ID. NO. 22 A A G A C C T A T G A C C C G T C A A T C A A T T G T A C A
SEQ. ID. NO. 23 T T T G A G G G C G T T T C T G G C C A T G T G G T C T T T

SEQ. ID. NO. 22 G T G G A A G A A A T G A C C G A G G C G G T G G A G G G C
SEQ. ID. NO. 23 G A T G C C A G C G G C T C C C G G A T G G C A T G G A C A

SEQ. ID. NO. 22 C A C A T C A C C A C G G A G A T T G T C A T G C T G A A C
SEQ. ID. NO. 23 C T T A T C G A G C A G C T A C A G G G C G G C A G C T A C

SEQ. ID. NO. 22 C C T G C C A A C A C C C G A A G C A T T T C C A A C A T G
SEQ. ID. NO. 23 A A G A A G A T C G G C T A C T A C G A C A G C A C C A A G

SEQ. ID. NO. 22 A C G T C A C A G G A A T T T G T G G A G A A A C T A A C C
SEQ. ID. NO. 23 G A T G A T C T T T C C T G G T C C A A A A C G G A C A A G

SEQ. ID. NO. 22 A A G C G G C T G A A A A G A C A C C C C G A G G A G A C T
SEQ. ID. NO. 23 T G G A T T G G A G G G T C T C C C C C A G C T G A C C A G

SEQ. ID. NO. 22 G G A G G C T T C C A G G A G G C A C C A C T G G C C T A T
SEQ. ID. NO. 23 A C C T T G G T C A T C A A G A C A T T C C G T T T C C T G

SEQ. ID. NO. 22 G A T G C T A T C T G G G C C T T G G C T T T G G C C T T G
SEQ. ID. NO. 23 T C T C A G A A A C T C T T T A T C T C C G T C T C A G T T

SEQ. ID. NO. 22 A A C A A G A C G T C T G G A G G A G G T G G T C G T T C C
SEQ. ID. NO. 23 C T C T C C A G C C T G G G C A T T G T T C T T G C T G T T

SEQ. ID. NO. 22 G G C G T G C G C C T G G A G G A C T T T A A C T A C A A C
SEQ. ID. NO. 23 G T C T G T C T G T C C T T T A A C A T C T A C A A C T C C

SEQ. ID. NO. 22 A A C C A G A C C A T T A C A G A C C A G A T C T A C C G G
SEQ. ID. NO. 23 C A C G T T C G T T A T A T C C A G A A C T C C C A G C C C

FIGURE 6e

SEQ. ID. NO. 22 G C C A T G A A C T C C T C C T T T G A G G G C G T T
SEQ. ID. NO. 23 A A C C T G A A C A A T C T G A C T G C T G T G G G C T G C

SEQ. ID. NO. 22 T C T G G C C A T G T G G T C T T T G A T G C C A G C G G C
SEQ. ID. NO. 23 T C A C T G G C A C T G G C T G C T G T C T T C C C T C T C

SEQ. ID. NO. 22 T C C C G G A T G G C A T G G A C A C T T A T C G A G C A G
SEQ. ID. NO. 23 G G G C T G G A T G G T T A C C A C A T A G G G A G A A G C

SEQ. ID. NO. 22 C T A C A G G G C G G C A G C T A C A A G A A G A T C G G C
SEQ. ID. NO. 23 C A G T T C C C G T T T G T C T G C C A G G C C C G C C T T

SEQ. ID. NO. 22 T A C T A C G A C A G C A C C A A G G A T G A T C T T T C C
SEQ. ID. NO. 23 T G G C T C T T G G G C T T G G G C T T T A G T C T G G G C

SEQ. ID. NO. 22 T G G T C C A A A A C G G A C A A G T G G A T T G G A G G G
SEQ. ID. NO. 23 T A T G G C T C T A T G T T C A C C A A G A T C T G G T G G

SEQ. ID. NO. 22 T C T C C C C A G C T G A C C A G A C C T T G G T C A T C
SEQ. ID. NO. 23 G T C C A C A C A G T C T T C A C G A A G A A G G A G G A G

SEQ. ID. NO. 22 A A G A C A T T C C G T T T C C T G T C T C A G A A A C T C
SEQ. ID. NO. 23 A A G A A G G A G T G G A G G A A G A C C C T A G A G C C C

SEQ. ID. NO. 22 T T T A T C T C C G T C T C A G T T C T C T C C A G C C T G
SEQ. ID. NO. 23 T G G A A A C T C T A T G C C A C T G T G G G C C T G C T G

SEQ. ID. NO. 22 G G C A T T G T T C T T G C T G T T G T C T G T C T G T C C
SEQ. ID. NO. 23 G T G G G C A T G G A T G T C C T G A C T C T T G C C A T C

SEQ. ID. NO. 22 T T T A A C A T C T A C A A C T C C C A C G T T C G T T A T
SEQ. ID. NO. 23 T G G C A G A T T G T G G A C C C C T T G C A C C G A A C C

SEQ. ID. NO. 22 A T C C A G A A C T C C C A G C C C A A C C T G A A C A A T
SEQ. ID. NO. 23 A T T G A G A C T T T T G C C A A G G A G G A A C C A A A G

SEQ. ID. NO. 22 C T G A C T G C T G T G G G C T G C T C A C T G G C A C T G
SEQ. ID. NO. 23 G A A G A C A T C G A T G T C T C C A T T C T G C C C C A G

FIGURE 6f

SEQ. ID. NO. 22 G C T G C T G T C T T C C C T C T C G G G C T G G A T G G T
SEQ. ID. NO. 23 T T G G A G C A C T G C A G C T C C A A G A A G A T G A A T

SEQ. ID. NO. 22 T A C C A C A T A G G G A G A A G C C A G T T C C C G T T T
SEQ. ID. NO. 23 A C G T G G C T T G G C A T T T T C T A T G G T T A C A A G

SEQ. ID. NO. 22 G T C T G C C A G G C C C G C C T T T G G C T C T T G G G C
SEQ. ID. NO. 23 G G G C T G C T G C T G C T G C T G G G A A T C T T T C T T

SEQ. ID. NO. 22 T T G G G C T T T A G T C T G G G C T A T G G C T C T A T G
SEQ. ID. NO. 23 G C T T A C G A A A C C A A G A G C G T G T C C A C T G A A

SEQ. ID. NO. 22 T T C A C C A A G A T C T G G T G G G T C C A C A C A G T C
SEQ. ID. NO. 23 A A G A T C A A T G A C C A C A G G G C C G T G G G C A T G

SEQ. ID. NO. 22 T T C A C G A A G A A G G A G G A G A A G A A G G A G T G G
SEQ. ID. NO. 23 G C T A T C T A C A A T G T C G C G G T C C T G T G T C T C

SEQ. ID. NO. 22 A G G A A G A C C C T A G A G C C C T G G A A A C T C T A T
SEQ. ID. NO. 23 A T C A C T G C T C C T G T G A C C A T G A T C C T T T C C

SEQ. ID. NO. 22 G C C A C T G T G G G C C T G C T G G T G G G C A T G G A T
SEQ. ID. NO. 23 A G T C A G C A G G A C G C A G C C T T T G C C T T T G C C

SEQ. ID. NO. 22 G T C C T G A C T C T T G C C A T C T G G C A G A T T G T G
SEQ. ID. NO. 23 T C T C T G G C C A T C G T G T T C T C T T C C T A C A T C

SEQ. ID. NO. 22 G A C C C C T T G C A C C G A A C C A T T G A G A C T T T T
SEQ. ID. NO. 23 A C T C T G G T T G T G C T C T T T G T G C C C A A G A T G

SEQ. ID. NO. 22 G C C A A G G A G G A A C C A A A G G A A G A C A T C G A T
SEQ. ID. NO. 23 C G C A G G C T G A T C A C C C G A G G G G A A T G G C A G

SEQ. ID. NO. 22 G T C T C C A T T C T G C C C C A G T T G G A G C A C T G C
SEQ. ID. NO. 23 T C T G A A A C G C A G G A C A C C A T G A A A A C A G G A

SEQ. ID. NO. 22 A G C T C C A A G A A G A T G A A T A C G T G G C T T G G C
SEQ. ID. NO. 23 T C A T C C A C C A A C A A C A A C G A G G A A G A G A A G

FIGURE 6c

SEQ. ID. NO. 22 A T T T T C T A T G G T T A C A A G G G G C T G C T G C T G
SEQ. ID. NO. 23 T C C C G A C T G T T G G A G A A G G A A A A C C G A G A A

SEQ. ID. NO. 22 C T G C T G G G A A T C T T T C T T G C T T A C G A A A C C
SEQ. ID. NO. 23 C T G G A A A A G A T C A T C G C T G A G A A A G A G G A G

SEQ. ID. NO. 22 A A G A G C G T G T C C A C T G A A A A G A T C A A T G A C
SEQ. ID. NO. 23 C G C G T C T C T G A A C T G C G C C A T C A G C T C C A G

SEQ. ID. NO. 22 C A C A G G G C C G T G G G C A T G G C T A T C T A C A A T
SEQ. ID. NO. 23 T C T C G G C A G C A A C T C C G C T C A C G G C G C C A C

SEQ. ID. NO. 22 G T C G C G G T C C T G T G T C T C A T C A C T G C T C C T
SEQ. ID. NO. 23 C C C C C A A C A C C C C C A G A T C C C T C T G G G G G C

SEQ. ID. NO. 22 G T G A C C A T G A T C C T T T C C A G T C A G C A G G A C
SEQ. ID. NO. 23 C T T C C C A G G G G A C C C T C T G A G C C C C C T G A C

SEQ. ID. NO. 22 G C A G C C T T T G C C T T T G C C T C T C T G G C C A T C
SEQ. ID. NO. 23 C G G C T T A G C T G T G A T G G G A G T C G A G T A C A T

SEQ. ID. NO. 22 G T G T T C T C T T C C T A C A T C A C T C T G G T T G T G
SEQ. ID. NO. 23 T T G C T T T A C A A G

SEQ. ID. NO. 22 C T C T T T G T G C C C A A G A T G C G C A G G C T G A T C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 A C C C G A G G G G A A T G G C A G T C T G A A A C G C A G
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A C A C C A T G A A A A C A G G A T C A T C C A C C A A C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 A A C A A C G A G G A A G A G A A G T C C C G A C T G T T G
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A G A A G G A A A A C C G A G A A C T G G A A A A G A T C
SEQ. ID. NO. 23

FIGURE 61.

SEQ. ID. NO. 22 A T C G C T G A G A A A G A G G A G C G C G T C T C T G A A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C T G C G C C A T C A G C T C C A G T C T C G G C A G C A A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C T C C G C T C A C G G C G C C A C C C C C C A A C A C C C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C C A G A T C C C T C T G G G G G C C T T C C C A G G G G A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C C C T C T G A G C C C C C T G A C C G G C T T A G C T G T
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A T G G G A G T C G A G T A C A T T T G C T T T A C A A G
SEQ. ID. NO. 23

FIGURE 7a

SEQ. ID. NO. 24 M L L L L V P L F L R P L G A G G A Q T P N A T S E G C Q
SEQ. ID. NO. 25 M G P G G P C T P V G W P L P L L L V M A A G V A P V W A S

SEQ. ID. NO. 24 I I H P P W E G G I R Y R G L T R D Q V K A I N F L P V D Y
SEQ. ID. NO. 25 H S P H L P R P H P R V P P H P S S E R R A V Y I G A L F P

SEQ. ID. NO. 24 E I E Y V C R G E R E V V G P K V R K C L A N G S W T D M D
SEQ. ID. NO. 25 M S G G W P G G Q A C Q P A V E M A L E D V N S R R D I L P

SEQ. ID. NO. 24 T P S R C V R I C S K S Y L T L E N G K V F L T G G D L P A
SEQ. ID. NO. 25 D Y E L K L I H H D S K C D P G Q A T K Y L Y E L L Y N D P

SEQ. ID. NO. 24 L D G A R V E F R C D P D F H L V G S S R S V C S Q G Q W S
SEQ. ID. NO. 25 I K I I L M P G C S S V S T L V A E A A R M W N L I V L S Y

SEQ. ID. NO. 24 T P K P H C Q V N R T P H S E R R A V Y I G A L F P M S G G
SEQ. ID. NO. 25 G S S S P A L S N R Q R F P T F F R T H P S A T L H N P T R

SEQ. ID. NO. 24 W P G G Q A C Q P A V E M A L E D V N S R R D I L P D Y E L
SEQ. ID. NO. 25 V K L F E K W G W K K I A T I Q Q T T E V F T S T L D D L E

SEQ. ID. NO. 24 K L I H H D S K C D P G Q A T K Y L Y E L L Y N D P I K I I
SEQ. ID. NO. 25 E R V K E A G I E I T F R Q S F F S D P A V P V K N L K R Q

SEQ. ID. NO. 24 L M P G C S S V S T L V A E A A R M W N L I V L S Y G S S S
SEQ. ID. NO. 25 D A R I I V G L F Y E T E A R K V F C E V Y K E R L F G K K

SEQ. ID. NO. 24 P A L S N R Q R F P T F F R T H P S A T L H N P T R V K L F
SEQ. ID. NO. 25 Y V W F L I G W Y A D N W F K T Y D P S I N C T V E E M T E

SEQ. ID. NO. 24 E K W G W K K I A T I Q Q T T E V F T S T L D D L E E R V K
SEQ. ID. NO. 25 A V E G H I T T E I V M L N P A N T R S I S N M T S Q E F V

SEQ. ID. NO. 24 E A G I E I T F R Q S F F S D P A V P V K N L K R Q D A R I
SEQ. ID. NO. 25 E K L T K R L K R H P E E T G G F Q E A P L A Y D A I W A L

FIGURE 71

SEQ. ID. NO. 24 I V G L F Y E T E A R K V F C E V Y K E R L F G K K Y V W F
SEQ. ID. NO. 25 A L A L N K T S G G G G R S G V R L E D F N Y N N Q T I T D

SEQ. ID. NO. 24 L I G W Y A D N W F K T Y D P S I N C T V E E M T E A V E G
SEQ. ID. NO. 25 Q I Y R A M N S S S F E G V S G H V V F D A S G S R M A W T

SEQ. ID. NO. 24 H I T T E I V M L N P A N T R S I S N M T S Q E F V E K L T
SEQ. ID. NO. 25 L I E Q L Q G G S Y K K I G Y Y D S T K D D L S W S K T D K

SEQ. ID. NO. 24 K R L K R H P E E T G G F Q E A P L A Y D A I W A L A L A L
SEQ. ID. NO. 25 W I G G S P P A D Q I L V I K T F R F L S Q K L F I S V S V

SEQ. ID. NO. 24 N K T S G G G G R S G V R L E D F N Y N N Q T I T D Q I Y R
SEQ. ID. NO. 25 L S S L G I V L A V V C L S F N I Y N S H V R Y I Q N S Q P

SEQ. ID. NO. 24 A M N S S S F E G V S G H V V F D A S G S R M A W T L I E Q
SEQ. ID. NO. 25 N L N N L T A V G C S L A L A A V F P L G L D G Y H I G R S

SEQ. ID. NO. 24 L Q G G S Y K K I G Y Y D S T K D D L S W S K T D K W I G G
SEQ. ID. NO. 25 Q F P F V C Q A R L W L L G L G F S L G Y G S M F T K I W W

SEQ. ID. NO. 24 S P P A D Q I L V I K T F R F L S Q K L F I S V S V L S S L
SEQ. ID. NO. 25 V H T V F T K K E E K K E W R K T L E P W K L Y A T V G L L

SEQ. ID. NO. 24 G I V L A V V C L S F N I Y N S H V R Y I Q N S Q P N L N N
SEQ. ID. NO. 25 V G M D V L T L A I W Q I V D P L H R T I E T F A K E E P K

SEQ. ID. NO. 24 L T A V G C S L A L A A V F P L G L D G Y H I G R S Q F P F
SEQ. ID. NO. 25 E D I D V S I L P Q L E H C S S K K M N T W L G I F Y G Y K

SEQ. ID. NO. 24 V C Q A R L W L L G L G F S L G Y G S M F T K I W W V H T V
SEQ. ID. NO. 25 G L L L L L G I F L A Y E T K S V S T E K I N D H R A V G M

SEQ. ID. NO. 24 F T K K E E K K E W R K T L E P W K L Y A T V G L L V G M D
SEQ. ID. NO. 25 A I Y N V A V L C L I T A P V T M I L S S Q Q D A A F A F A

SEQ. ID. NO. 24 V L T L A I W Q I V D P L H R T I E T F A K E E P K E D I D
SEQ. ID. NO. 25 S L A I V F S S Y I T L V V L F V P K M R R L I T R G E W Q

FIGURE 7c

SEQ. ID. NO. 24 V S I L P Q L E H C S S K K M N T W L G I F Y G Y K G L L L
SEQ. ID. NO. 25 S E T Q D T M K T G S S T N N N E E E K S R L L E K E N R E

SEQ. ID. NO. 24 L L G I F L A Y E T K S V S T E K I N D H R A V G M A I Y N
SEQ. ID. NO. 25 L E K I I A E K E E R V S E L R H Q L Q S R Q Q L R S R R H

SEQ. ID. NO. 24 V A V L C L I T A P V T M I L S S Q Q D A A F A F A S L A I
SEQ. ID. NO. 25 P P T P P D P S G G L P R G P S E P P D R L S C D G S R V H

SEQ. ID. NO. 24 V F S S Y I T L V V L F V P K M R R L I T R G E W Q S E T Q
SEQ. ID. NO. 25 L L Y K

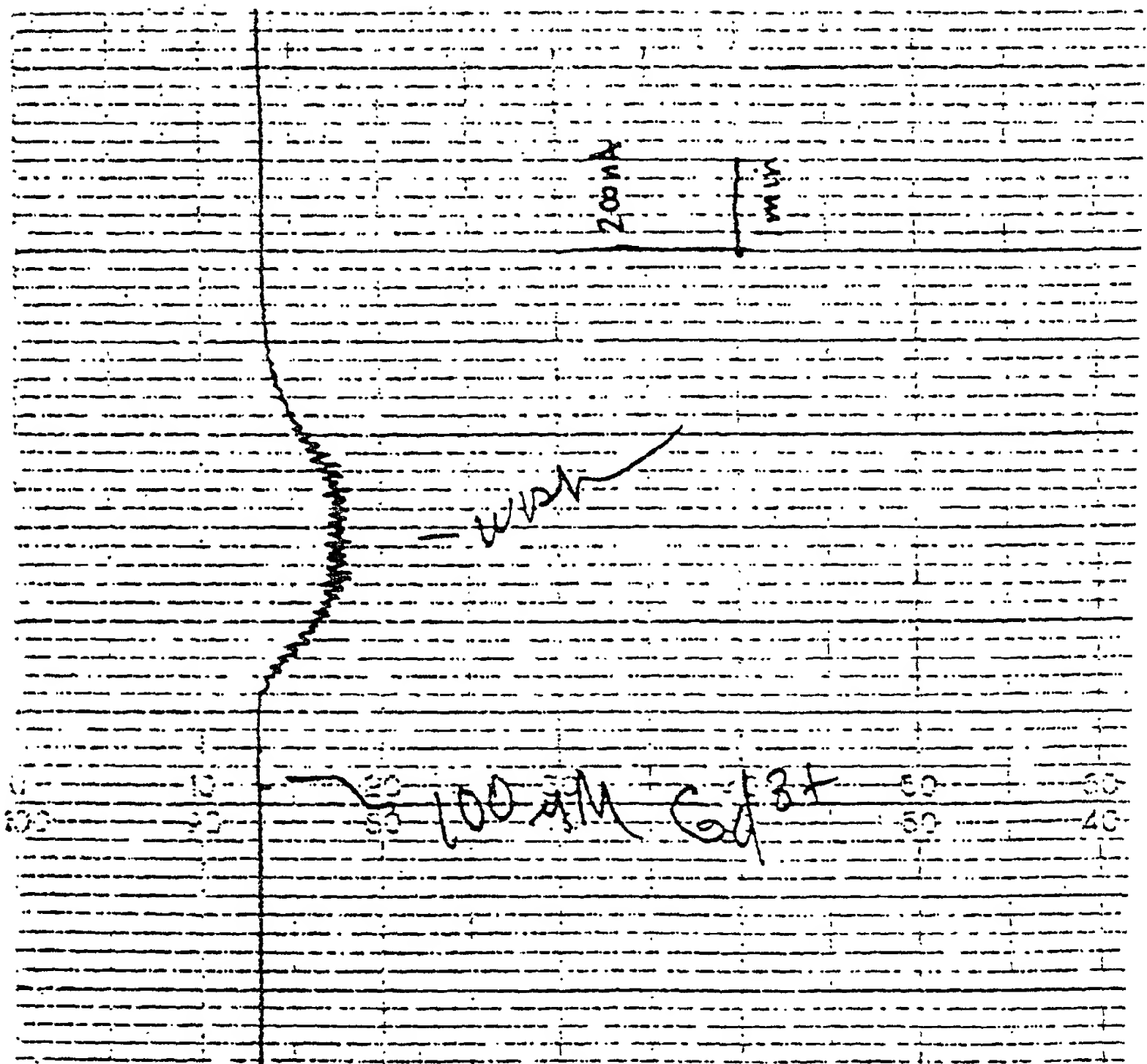
SEQ. ID. NO. 24 D T M K T G S S T N N N E E E K S R L L E K E N R E L E K I
SEQ. ID. NO. 25

SEQ. ID. NO. 24 I A E K E E R V S E L R H Q L Q S R Q Q L R S R R H P P T P
SEQ. ID. NO. 25

SEQ. ID. NO. 24 P D P S G G L P R G P S E P P D R L S C D G S R V H L L Y K
SEQ. ID. NO. 25

FIGURE 8

STATION NO. 122000



ClustalW Formatted Alignments

SEQ. ID. NO. 38 A T G G T A T G C G A G G G A A A G C G A T C A G
 SEQ. ID. NO. 34 A T G G G A T C G C T G C T T G C G C T C C C G G
 SEQ. ID. NO. 30 A T G G C A T T T T A T A G C T G C T G C T G G G
 SEQ. ID. NO. 26 A T G G G A T C G C T G C T T G C G C T C C T G G

SEQ. ID. NO. 38 C C T C T T G C C C T T G T T T C T T C C T C T T
 SEQ. ID. NO. 34 C A C T G C T G C T G C T G T G G G G T G C T G T
 SEQ. ID. NO. 30 T C C T C T T G G C A C T C A C C T G G C A C A C
 SEQ. ID. NO. 26 C A C T G C T G C C G C T G T G G G G T G C T G T

SEQ. ID. NO. 38 G A C C G C C A A G T T C T A C T G G A T C C T C
 SEQ. ID. NO. 34 G G C T G A G G G C C C A G C C A A G A A G G T G
 SEQ. ID. NO. 30 C T C T G C C T A C G G G C C A G A C C A G C G A
 SEQ. ID. NO. 26 G G C T G A G G G C C C A G C C A A G A A G G T G

SEQ. ID. NO. 38 A C A A T G A T G C A A A G A A C T C A C A G C C
 SEQ. ID. NO. 34 C T G A C C C T G G A G G G A G A C T T G G T G C
 SEQ. ID. NO. 30 G C C C A A A A G A A G G G G G A C A T T A T C C
 SEQ. ID. NO. 26 C T G A C C C T G G A G G G A G A C T T G G T G C

SEQ. ID. NO. 38 A G G A G T A T G C C C A T T C C A T A C G G G T
 SEQ. ID. NO. 34 T G G G T G G G C T G T T C C C A G T G C A C C A
 SEQ. ID. NO. 30 T T G G G G G G C T C T T T C C T A T T C A T T T
 SEQ. ID. NO. 26 T G G G T G G G C T G T T C C C A G T G C A C C A

SEQ. ID. NO. 38 G G A T G G G G A C A T T A T T T T G G G G G G T
 SEQ. ID. NO. 34 G A A G G G C G G C C C A G C A G A G G A C T G T
 SEQ. ID. NO. 30 T G G A G T A G C A G C T A A A G A T C A A G A T
 SEQ. ID. NO. 26 G A A G G G C G G C C C A G C A G A G G A C T G T

SEQ. ID. NO. 38 C T C T T C C C T G T C C A C G C A A A G G G A G
 SEQ. ID. NO. 34 G G T C C T G T C A A T G A G C A C C G T G G C A
 SEQ. ID. NO. 30 C T C A A A T C A A G G C C G G A G T C T G T G G
 SEQ. ID. NO. 26 G G T C C T G T C A A T G A G C A C C G T G G C A

SEQ. ID. NO. 38 A G A G A G G G G T G C C T T G T G G G G A G C T
 SEQ. ID. NO. 34 T C C A G C G C C T G G A G G C C A T G C T T T T
 SEQ. ID. NO. 30 A A T G T A T C A G G T A T A A T T T C C G T G G
 SEQ. ID. NO. 26 T C C A G C G C C T G G A G G C C A T G C T T T T

Figure 9a

SEQ. ID. NO. 38 G A A G A A G G A A A A G G G G A T T C A C A G A
 SEQ. ID. NO. 34 T G C A C T G G A C C G C A T C A A C C G T G A C
 SEQ. ID. NO. 30 G T T T C G C T G G T T A C A G G C T A T G A T A
 SEQ. ID. NO. 26 T G C A C T G G A C C G C A T C A A C C G T G A C

SEQ. ID. NO. 38 C T G G A G G C C A T G C T T T A T G C A A T T G
 SEQ. ID. NO. 34 C C G C A C C T G C T G C C T G G C G T G C G C C
 SEQ. ID. NO. 30 T T T G C C A T A G A G G A G A T A A A C A G C A
 SEQ. ID. NO. 26 C C G C A C C T G C T G C C T G G C G T G C G C C

SEQ. ID. NO. 38 A C C A G A T T A A C A A G G A C C C T G A T C T
 SEQ. ID. NO. 34 T G G G T G C A C A C A T C C T C G A C A G T T G
 SEQ. ID. NO. 30 G C C C A G C C C T T C T T C C C A A C T T G A C
 SEQ. ID. NO. 26 T G G G T G C A C A C A T C C T C G A C A G T T G

SEQ. ID. NO. 38 C C T T T C C A A C A T C A C T C T G G G T G T C
 SEQ. ID. NO. 34 C T C C A A G G A C A C A C A T G C G C T G G A G
 SEQ. ID. NO. 30 G C T G G G A T A C A G G A T A T T T G A C A C T
 SEQ. ID. NO. 26 C T C C A A G G A C A C A C A T G C G C T G G A G

SEQ. ID. NO. 38 C G C A T C C T C G A C A C G T G C T C T A G G G
 SEQ. ID. NO. 34 C A G G C A C T G G A C T T T G T G C G T G C C T
 SEQ. ID. NO. 30 T G C A A C A C C G T T T C T A A G G C C T T G G
 SEQ. ID. NO. 26 C A G G C A C T G G A C T T T G T G C G T G C C T

SEQ. ID. NO. 38 A C A C C T A T G C T T T G G A G C A G T C T C T
 SEQ. ID. NO. 34 C A C T C A G C C G T G G T G C T G A T G G C T C
 SEQ. ID. NO. 30 A A G C C A C C C T G A G T T T T G T T G C T C A
 SEQ. ID. NO. 26 C A C T C A G C C G T G G T G C T G A T G G A T C

SEQ. ID. NO. 38 A A C A T T C G T G C A G G C A T T A A T A G A G
 SEQ. ID. NO. 34 A C G C C A C A T C T G C C C C G A C G G C T C T
 SEQ. ID. NO. 30 A A A C A A A A T T G A T T C T T T G A A C C T T
 SEQ. ID. NO. 26 A C G C C A C A T C T G C C C C G A C G G C T C T

SEQ. ID. NO. 38 A A A G A T G C T T C G G A T G T G A A G T G T G
 SEQ. ID. NO. 34 T A T G C G A C C C A T G G T G A T G C T C C C A
 SEQ. ID. NO. 30 G A T G A G T T C T G C A A C T G C T C A G A G C
 SEQ. ID. NO. 26 T A T G C G A C C C A T G G T G A T G C T C C C A

Figure 9b

SEQ. ID. NO. 38 C T A A T G G A G A T C C A C C C A T T T T C A C
 SEQ. ID. NO. 34 C T G C C A T C A C T G G T G T T A T T G G C G G
 SEQ. ID. NO. 30 A C A T T C C C T C T A C G A T T G C T G T G G T
 SEQ. ID. NO. 26 C T G C C A T C A C T G G T G T T A T T G G C G G

SEQ. ID. NO. 38 C A A G C C C G A C A A G A T T T C T G G C G T C
 SEQ. ID. NO. 34 T T C C T A C A G T G A T G T C T C C A T C C A G
 SEQ. ID. NO. 30 G G G A G C A A C T G G C T C A G G C G T C T C C
 SEQ. ID. NO. 26 T T C C T A C A G T G A T G T C T C C A T C C A G

SEQ. ID. NO. 38 A T A G G T G C T G C A G C A A G C T C C G T G T
 SEQ. ID. NO. 34 G T G G C C A A C C T C T T G A G G C T A T T T C
 SEQ. ID. NO. 30 A C G G C A G T G G C A A A T C T G C T G G G G C
 SEQ. ID. NO. 26 G T G G C C A A C C T C T T G A G G C T A T T T C

SEQ. ID. NO. 38 C C A T C A T G G T T G C T A A C A T T T T A A G
 SEQ. ID. NO. 34 A G A T C C C A C A G A T T A G C T A C G C C T C
 SEQ. ID. NO. 30 T C T T C T A C A T T C C C C A G G T C A G T T A
 SEQ. ID. NO. 26 A G A T C C C A C A G A T T A G C T A C G C C T C

SEQ. ID. NO. 38 A C T T T T T A A G A T A C C T C A A A T C A G C
 SEQ. ID. NO. 34 T A C C A G T G C C A A G C T G A G T G A C A A G
 SEQ. ID. NO. 30 T G C C T C C T C C A G C A G A C T C C T C A G C
 SEQ. ID. NO. 26 T A C C A G T G C C A A G C T G A G T G A C A A G

SEQ. ID. NO. 38 T A T G C A T C C A C A G C C C C A G A G C T A A
 SEQ. ID. NO. 34 T C C C G C T A T G A C T A C T T T G C C C G C A
 SEQ. ID. NO. 30 A A C A A G A A T C A A T T C A A G T C T T T C C
 SEQ. ID. NO. 26 T C C C G C T A T G A C T A C T T T G C C C G C A

SEQ. ID. NO. 38 G T G A T A A C A C C A G G T A T G A C T T T T T
 SEQ. ID. NO. 34 C A G T G C C T C C T G A C T T C T T C C A A G C
 SEQ. ID. NO. 30 T C C G A A C C A T C C C C A A T G A T G A G C A
 SEQ. ID. NO. 26 C A G T G C C T C C T G A C T T C T T C C A A G C

SEQ. ID. NO. 38 C T C T C G A G T G G T T C C G C C T G A C T C C
 SEQ. ID. NO. 34 C A A G G C C A T G G C T G A G A T T C T C C G C
 SEQ. ID. NO. 30 C C A G G C C A C T G C C A T G G C A G A C A T C
 SEQ. ID. NO. 26 C A A G G C C A T G G C T G A G A T T C T C C G C

Figure 9c

SEQ. ID. NO. 38 T A C C A A G C C C A A G C C A T G G T G G A C A
 SEQ. ID. NO. 34 T T C T T C A A C T G G A C C T A T G T G T C C A
 SEQ. ID. NO. 30 A T C G A G T A T T T C C G C T G G A A C T G G G
 SEQ. ID. NO. 26 T T C T T C A A C T G G A C C T A T G T G T C C A

SEQ. ID. NO. 38 T C G T G A C A G C A C T G G G A T G G A A T T A
 SEQ. ID. NO. 34 C T G T G G C G T C T G A G G G C G A C T A T G G
 SEQ. ID. NO. 30 T G G G C A C A A T T G C A G C T G A T G A C G A
 SEQ. ID. NO. 26 C T G A G G C C T C T G A G G G C G A C T A T G G

SEQ. ID. NO. 38 T G T T T C G A C A C T G G C T T C T G A G G G G
 SEQ. ID. NO. 34 C G A G A C A G G C A T T G A G G C C T T T G A G
 SEQ. ID. NO. 30 C T A T G G G C G G C C G G G G A T T G A G A A A
 SEQ. ID. NO. 26 C G A G A C A G G C A T T G A G G C C T T T G A G

SEQ. ID. NO. 38 A A C T A T G G T G A G A G C G G T G T G G A G G
 SEQ. ID. NO. 34 C T A G A G G C T C G T G C C C G C A A C A T C T
 SEQ. ID. NO. 30 T T C C G A G A G G A A G C T G A G G A A A G G G
 SEQ. ID. NO. 26 C T A G A G G C T C G T G C C C G C A A C A T C T

SEQ. ID. NO. 38 C C T T C A C C C A G A T C T C G A G G G A G A T
 SEQ. ID. NO. 34 G T G T G G C C A C C T C G G A G A A A G T G G G
 SEQ. ID. NO. 30 A T A T C T G C A T C G A C T T C A G T G A A C T
 SEQ. ID. NO. 26 G T G T G G C C A C C T C G G A G A A A G T G G G

SEQ. ID. NO. 38 T G G T G G T G T T T G C A T T G C T C A G T C A
 SEQ. ID. NO. 34 C C G T G C C A T G A G C C G C G C G G C C T T T
 SEQ. ID. NO. 30 C A T C T C C C A G T A C T C T G A T G A G G A A
 SEQ. ID. NO. 26 C C G T G C C A T G A G C C G C G C G G C C T T T

SEQ. ID. NO. 38 C A G A A A A T C C C A C G T G A A C C A A G A C
 SEQ. ID. NO. 34 G A G G G T G T G G T G C G A G C C C T G C T G C
 SEQ. ID. NO. 30 G A G A T C C A G C A T G T G G T A G A G G T G A
 SEQ. ID. NO. 26 G A G G G T G T G G T G C G A G C C C T G C T G C

SEQ. ID. NO. 38 C T G G A G A A T T T G A A A A A A T T A T C A A
 SEQ. ID. NO. 34 A G A A G C C C A G T G C C C G C G T G G C T G T
 SEQ. ID. NO. 30 T T C A A A A T T C C A C G G C C A A A G T C A T
 SEQ. ID. NO. 26 A G A A G C C C A G T G C C C G C G T G G C T G T

Figure 9d

SEQ. ID. NO. 38 A C G C C T G C T A G A A A C A C C T A A T G C T
 SEQ. ID. NO. 34 C C T G T T C A C C C G T T C T G A G G A T G C C
 SEQ. ID. NO. 30 C G T G G T T T T C T C C A G T G G C C C A G A T
 SEQ. ID. NO. 26 C C T G T T C A C C C G T T C T G A G G A T G C C

SEQ. ID. NO. 38 C G A G C A G T G A T T A T G T T T G C C A A T G
 SEQ. ID. NO. 34 C G G G A G C T G C T T G C T G C C A G C C A G C
 SEQ. ID. NO. 30 C T T G A G C C C C T C A T C A A G G A G A T T G
 SEQ. ID. NO. 26 C G G G A G C T G C T T G C T G C C A G C C A G C

SEQ. ID. NO. 38 A G G A T G A C A T C A G G A G G A T A T T G G A
 SEQ. ID. NO. 34 G C C T C A A T G C C A G C T T C A C C T G G G T
 SEQ. ID. NO. 30 T C C G G C G C A A T A T C A C G G G C A A G A T
 SEQ. ID. NO. 26 G C C T C A A T G C C A G C T T C A C C T G G G T

SEQ. ID. NO. 38 A G C A G C A A A A A A A C T A A A C C A A A G T
 SEQ. ID. NO. 34 G G C C A G T G A T G G T T G G G G G G C C C T G
 SEQ. ID. NO. 30 C T G G C T G G C C A G C G A G G C C T G G G C C
 SEQ. ID. NO. 26 G G C C A G T G A T G G T T G G G G G G C C C T G

SEQ. ID. NO. 38 G G G C A T T T T C T C T G G A T T G G C T C A G
 SEQ. ID. NO. 34 G A G A G T G T G G T G G C A G G C A G T G A G G
 SEQ. ID. NO. 30 A G C T C C T C C C T G A T C G C C A T G C C T C
 SEQ. ID. NO. 26 G A G A G T G T G G T G G C A G G C A G T G A G G

SEQ. ID. NO. 38 A T A G T T G G G G A T C C A A A A T A G C A C C
 SEQ. ID. NO. 34 G G G C T G C T G A G G G T G C T A T C A C C A T
 SEQ. ID. NO. 30 A G T A C T T C C A C G T G G T T G G C G G C A C
 SEQ. ID. NO. 26 G G G C T G C T G A G G G T G C T A T C A C C A T

SEQ. ID. NO. 38 T G T C T A T C A G C A A G A G G A G A T T G C A
 SEQ. ID. NO. 34 C G A G C T G G C C T C C T A C C C C A T C A G T
 SEQ. ID. NO. 30 C A T T G G A T T C G C T C T G A A G G C T G G G
 SEQ. ID. NO. 26 C G A G C T G G C C T C C T A C C C C A T C A G T

SEQ. ID. NO. 38 G A A G G G G C T G T G A C A A T T T T G C C C A
 SEQ. ID. NO. 34 G A C T T T G C C T C C T A C T T C C A G A G C C
 SEQ. ID. NO. 30 C A G A T C C C A G G C T T C C G G G A A T T C C
 SEQ. ID. NO. 26 G A C T T T G C C T C C T A C T T C C A G A G C C

Figure 9e

SEQ. ID. NO. 38 A A C G A G C A T C A A T T G A T G G A T T T G A
 SEQ. ID. NO. 34 T G G A C C C T T G G A A C A A C A G C C G G A A
 SEQ. ID. NO. 30 T G A A G A A G G T C C A T C C C A G G A A G T C
 SEQ. ID. NO. 26 T G G A C C C T T G G A A C A A C A G C C G G A A

SEQ. ID. NO. 38 T C G A T A C T T T A G A A G C C G A A C T C T T
 SEQ. ID. NO. 34 C C C C T G G T T C C G T G A A T T C T G G G A G
 SEQ. ID. NO. 30 T G T C C A C A A T G G T T T T G C C A A G G A G
 SEQ. ID. NO. 26 C C C C T G G T T C C G T G A A T T C T G G G A G

SEQ. ID. NO. 38 G C C A A T A A T C G A A G A A A T G T G T G G T
 SEQ. ID. NO. 34 C A G A G G T T C C G C T G C A G C T T C C G G C
 SEQ. ID. NO. 30 T T T T G G G A A G A A A C A T T T A A C T G C C
 SEQ. ID. NO. 26 C A G A G G T T C C G C T G C A G C T T C C G G C

SEQ. ID. NO. 38 T T G C A G A A T T C T G G G A G G A G A A T T T
 SEQ. ID. NO. 34 A G C G A G A C T G C G C A G C C C A C T C T C T
 SEQ. ID. NO. 30 A C C T C C A A G A A G G T G C A A A A G G A C C
 SEQ. ID. NO. 26 A G C G A G A C T G C G C A G C C C A C T C T C T

SEQ. ID. NO. 38 T G G C T G C A A G T T A G G A T C A C A T G G G
 SEQ. ID. NO. 34 C C G G G C T G T G C C C T T T G A G C A G G A G
 SEQ. ID. NO. 30 T T T A C C T G T G G A C A C C T T T C T G A G A
 SEQ. ID. NO. 26 C C G G G C T G T G C C C T T T G A A C A G G A G

SEQ. ID. NO. 38 A A A A G G A A C A G T C A T A T A A A G A A A T
 SEQ. ID. NO. 34 T C C A A G A T C A T G T T T G T G G T C A A T G
 SEQ. ID. NO. 30 G G T C A C G A A G A A A G T G G C G A C A G G T
 SEQ. ID. NO. 26 T C C A A G A T C A T G T T T G T G G T C A A T G

SEQ. ID. NO. 38 G C A C A G G G C T G G A G C G A A T T G C T C G
 SEQ. ID. NO. 34 C A G T G T A C G C C A T G G C C C A T G C G C T
 SEQ. ID. NO. 30 T T A G C A A C A G C T C G A C A G C C T T C C G
 SEQ. ID. NO. 26 C A G T G T A C G C C A T G G C C C A T G C G C T

SEQ. ID. NO. 38 G G A T T C A T C T T A T G A A C A G G A A G G A
 SEQ. ID. NO. 34 C C A C A A C A T G C A C C G T G C C C T C T G C
 SEQ. ID. NO. 30 A C C C C T C T G T A C A G G G G A T G A G A A C
 SEQ. ID. NO. 26 C C A C A A C A T G C A C C G T G C C C T C T G C

Figure 9f

SEQ. ID. NO. 38 A A G G T C C A A T T T G T A A T T G A T G C T G
 SEQ. ID. NO. 34 C C C A A C A C C A C C C G G C T C T G T G A C G
 SEQ. ID. NO. 30 A T C A G C A G T G T C G A G A C C C C T T A C A
 SEQ. ID. NO. 26 C C C A A C A C C A C C C G G C T C T G T G A C G

SEQ. ID. NO. 38 T A T A T T C C A T G G C T T A C G C C C T G C A
 SEQ. ID. NO. 34 C G A T G C G G C C A G T T A A C G G G C G C C G
 SEQ. ID. NO. 30 T A G A T T A C A C G C A T T T A C G G A T A T C
 SEQ. ID. NO. 26 C G A T G C G G C C A G T T A A C G G G C G C C G

SEQ. ID. NO. 38 C A A T A T G C A C A A A G A T C T C T G C C C T
 SEQ. ID. NO. 34 C C T C T A C A A G G A C T T T G T G C T C A A C
 SEQ. ID. NO. 30 C T A C A A T G T G T A C T T A G C A G T C T A C
 SEQ. ID. NO. 26 C C T C T A C A A G G A C T T T G T G C T C A A C

SEQ. ID. NO. 38 G G A T A C A T T G G C C T T T G T C C A C G A A
 SEQ. ID. NO. 34 G T C A A G T T T G A T G C C C C C T T T C G C C
 SEQ. ID. NO. 30 T C C A T T G C C C A C G C C T T G C A A G A T A
 SEQ. ID. NO. 26 G T C A A G T T T G A T G C C C C C T T T C G C C

SEQ. ID. NO. 38 T G A G T A C C A T T G A T G G G A A A G A G C T
 SEQ. ID. NO. 34 C A G C T G A C A C C C A C A A T G A G G T C C G
 SEQ. ID. NO. 30 T A T A T A C C T G C T T A C C T G G G A G A G G
 SEQ. ID. NO. 26 C A G C T G A C A C C C A C A A T G A G G T C C G

SEQ. ID. NO. 38 A C T T G G T T A T A T T C G G G C T G T A A A T
 SEQ. ID. NO. 34 C T T T G A C C G C T T T G G T G A T G G T A T T
 SEQ. ID. NO. 30 G C T C T T C A C C A A T G G C T C C T G T G C A
 SEQ. ID. NO. 26 C T T T G A C C G C T T T G G T G A T G G T A T T

SEQ. ID. NO. 38 T T T A A T G G C A G T G C T G G C A C T C C T G
 SEQ. ID. NO. 34 G G C C G C T A C A A C A T C T T C A C C T A T C
 SEQ. ID. NO. 30 G A C A T C A A G A A A G T T G A G G C G T G G C
 SEQ. ID. NO. 26 G G C C G C T A C A A C A T C T T C A C C T A T C

SEQ. ID. NO. 38 T C A C T T T T A A T G A A A A C G G A G A T G C
 SEQ. ID. NO. 34 T G C G T G C A G G C A G T G G G C G C T A T C G
 SEQ. ID. NO. 30 A G G T C C T G A A G C A C C T A C G G C A T C T
 SEQ. ID. NO. 26 T G C G T G C A G G C A G T G G G C G C T A T C G

Figure 9g

SEQ. ID. NO. 38 T C C T G G A C G T T A T G A T A T C T T C C A G
 SEQ. ID. NO. 34 C T A C C A G A A G G T G G G C T A C T G G G C A
 SEQ. ID. NO. 30 A A A C T T T A C A A A C A A T A T G G G G G A G
 SEQ. ID. NO. 26 C T A C C A G A A G G T G G G C T A C T G G G C A

SEQ. ID. NO. 38 T A T C A A A T A A C C A A C A A A A G C A C A G
 SEQ. ID. NO. 34 G A A G G C T T G A C T C T G G A C A C C A G C C
 SEQ. ID. NO. 30 C A G G T G A C C T T T G A T G A G T G T G G T G
 SEQ. ID. NO. 26 G A A G G C T T G A C T C T G G A C A C C A G C C

SEQ. ID. NO. 38 A G T A C A A A G T C A T C G G C C A C T G G A C
 SEQ. ID. NO. 34 T C A T C C C A T G G G C C T C A C C C T C A G C
 SEQ. ID. NO. 30 A C C T G G T G G G G A A C T A T T C C A T C A T
 SEQ. ID. NO. 26 T C A T C C C A T G G G C C T C A C C G T C A G C

SEQ. ID. NO. 38 C A A T C A G C T T C A T C T A A A A G T G G A A
 SEQ. ID. NO. 34 C G G C C C C C T G C C C G C C T C T C G C T G C
 SEQ. ID. NO. 30 C A A C T G G C A C C T C T C C C C A G A G G A T
 SEQ. ID. NO. 26 C G G C C C C C T G G C C G C C T C T C G C T G C

SEQ. ID. NO. 38 G A C A T G C A G T G G G C T C A T A G A G A A C
 SEQ. ID. NO. 34 A G T G A G C C C T G C C T C C A G A A T G A G G
 SEQ. ID. NO. 30 G G C T C C A T C G T G T T T A A G G A A G T C G
 SEQ. ID. NO. 26 A G T G A G C C C T G C C T C C A G A A T G A G G

SEQ. ID. NO. 38 A T A C T C A C C C G G C G T C T G T C T G C A G
 SEQ. ID. NO. 34 T G A A G A G T G T G C A G C C G G G C G A A G T
 SEQ. ID. NO. 30 G G T A T T A C A A C G T C T A T G C C A A G A A
 SEQ. ID. NO. 26 T G A A G A G T G T G C A G C C G G G C G A A G T

SEQ. ID. NO. 38 C C T G C C G T G T A A G C C A G G G G A G A G G
 SEQ. ID. NO. 34 C T G C T G C T G G C T C T G C A T T C C G T G C
 SEQ. ID. NO. 30 G G G A G A A A G A C T C T T C A T C A A C G A G
 SEQ. ID. NO. 26 C T G C T G C T G G C T C T G C A T T C C G T G C

SEQ. ID. NO. 38 A A G A A A A C G G T G A A A G G G G T C C C T T
 SEQ. ID. NO. 34 C A G C C C T A T G A G T A C C G A T T G G A C G
 SEQ. ID. NO. 30 G A G A A A A T C C T G T G G A G T G G G T T C T
 SEQ. ID. NO. 26 C A G C C C T A T G A G T A C C G A T T G G A C G

Figure 9h

SEQ. ID. NO. 38 G C T G C T G G C A C T G T G A A C G C T G T G A
 SEQ. ID. NO. 34 A A T T C A C T T G C G C T G A T T G T G G C C T
 SEQ. ID. NO. 30 C C A G G G A G G T G C C C T T C T C C A A C T G
 SEQ. ID. NO. 26 A A T T C A C T T G C G C T G A T T G T G G C C T

SEQ. ID. NO. 38 A G G T T A C A A C T A C C A G G T G G A T G A G
 SEQ. ID. NO. 34 G G G C T A C T G G C C C A A T G C C A G C C T G
 SEQ. ID. NO. 30 C A G C C G A G A C T G C C T G G C A G G G A C C
 SEQ. ID. NO. 26 G G G C T A C T G G C C C A A T G C C A G C C T G

SEQ. ID. NO. 38 C T G T C C T G T G A A C T T T G C C C T C T G G
 SEQ. ID. NO. 34 A C T G G C T G C T T C G A A C T G C C C C A G G
 SEQ. ID. NO. 30 A G G A A A G G G A T C A T T G A G G G G G A G C
 SEQ. ID. NO. 26 A C T G G C T G C T T C G A A C T G C C C C A G G

SEQ. ID. NO. 38 A T C A G A G A C C C A A C A T G A A C C G C A C
 SEQ. ID. NO. 34 A G T A C A T C C G C T G G G G C G A T G C C T G
 SEQ. ID. NO. 30 C C A C C T G C T G C T T T G A G T G T G T G G A
 SEQ. ID. NO. 26 A G T A C A T C C G C T G G G G C G A T G C C T G

SEQ. ID. NO. 38 A G G C T G C C A G C T T A T C C C C A T C A T C
 SEQ. ID. NO. 34 G G C T G T G G G A C C T G T C A C C A T C G C C
 SEQ. ID. NO. 30 G T G T C C T G A T G G G G A G T A T A G T G A T
 SEQ. ID. NO. 26 G G C T G T G G G A C C T G T C A C C A T C G C C

SEQ. ID. NO. 38 A A A T T G G A G T G G C A T T C T C C C T G G G
 SEQ. ID. NO. 34 T G C C T C G G T G C C C T G G C C A C C C T C T
 SEQ. ID. NO. 30 G A G A C A G A T G C C A G T G C C T G T A A C A
 SEQ. ID. NO. 26 T G C C T C G G T G C C C T G G C C A C C C T G T

SEQ. ID. NO. 38 C T G T G G T G C C T G T G T T T G T T G C A A T
 SEQ. ID. NO. 34 T T G T G C T G G G T G T C T T T G T G C G G C A
 SEQ. ID. NO. 30 A G T G C C C A G A T G A C T T C T G G T C C A A
 SEQ. ID. NO. 26 T T G T G C T G G G T G T C T T T G T G C G G C A

SEQ. ID. NO. 38 A T T G G G A A T C A T C G C C A C C A C C T T T
 SEQ. ID. NO. 34 C A A T G C C A C A C C A G T G G T C A A G G C C
 SEQ. ID. NO. 30 T G A G A A C C A C A C C T C C T G C T T C G A A
 SEQ. ID. NO. 26 C A A T G C C A C A C C A G T G G T C A A G G C C

Figure 9i

SEQ. ID. NO. 38	G T G A T C G T G A C C T T T G T C C G C T A T A
SEQ. ID. NO. 34	T C A G G T C G G G A G C T C T G C T A C A T C C
SEQ. ID. NO. 30	C T G C C C C A G G A G T A C A T C C G C T G G G
SEQ. ID. NO. 26	T C A G G T C G G G A G C T C T G C T A C A T C C
SEQ. ID. NO. 38	A T G A C A C A C C T A T C G T G A G G G C T T C
SEQ. ID. NO. 34	T G C T G G G T G G T G T C T T C C T C T G C T A
SEQ. ID. NO. 30	G C G A T G C C T G G G C T G T G G G A C C T G T
SEQ. ID. NO. 26	T G C T G G G T G G T G T C T T C C T C T G C T A
SEQ. ID. NO. 38	A G G A C G C G A A C T T A G T T A C G T G C T C
SEQ. ID. NO. 34	C T G C A T G A C C T T C A T C T T C A T T G C C
SEQ. ID. NO. 30	C A C C A T C G C C T G C C T C G G T G C C C T G
SEQ. ID. NO. 26	C T G C A T G A C C T T C A T C T T C A T T G C C
SEQ. ID. NO. 38	C T A A C G G G G A T T T T T C T C T G T T A T T
SEQ. ID. NO. 34	A A G C C A T C C A C G G C A G T G T G T A C C T
SEQ. ID. NO. 30	G C C A C C C T G T T T G T G C T G G G T G T C T
SEQ. ID. NO. 26	A A G C C A T C C A C G G C A G T G T G T A C C T
SEQ. ID. NO. 38	C A A T C A C G T T T T T A A T G A T T G C A G C
SEQ. ID. NO. 34	T A C G G C G T C T T G G T T T G G G C A C T G C
SEQ. ID. NO. 30	T T G T G C G G C A C A A T G C C A C A C C A G T
SEQ. ID. NO. 26	T A C G G C G T C T T G G T T T G G G C A C T G C
SEQ. ID. NO. 38	A C C A G A T A C A A T C A T A T G C T C C T T C
SEQ. ID. NO. 34	C T T C T C T G T C T G C T A C T C A G C C C T G
SEQ. ID. NO. 30	G G T C A A G G C C T C A G G T C G G G A G C T C
SEQ. ID. NO. 26	C T T C T C T G T C T G C T A C T C A G C C C T G
SEQ. ID. NO. 38	C G A C G G G T C T T C C T A G G A C T T G G C A
SEQ. ID. NO. 34	C T C A C C A A G A C C A A C C G C A T T G C A C
SEQ. ID. NO. 30	T G C T A C A T C C T G C T G G G T G G T G T C T
SEQ. ID. NO. 26	C T C A C C A A G A C C A A C C G C A T T G C A C
SEQ. ID. NO. 38	T G T G T T T C A G C T A T G C A G C C C T T C T
SEQ. ID. NO. 34	G C A T C T T C G G T G G G G C C C G G G A G G G
SEQ. ID. NO. 30	T C C T C T G C T A C T G C A T G A C C T T C A T
SEQ. ID. NO. 26	G C A T C T T C G G T G G G G C C C G G G A G G G

Figure 9j

SEQ. ID. NO. 38 G A C C A A A A C A A A C C G T A T C C A C C G A
 SEQ. ID. NO. 34 T G C C C A G C G G C C A C G C T T C A T C A G T
 SEQ. ID. NO. 30 C T T C A T T G C C A A G C C A T C C A C G G C A
 SEQ. ID. NO. 26 T G C C C A G C G G C C A C G C T T C A T C A G T

SEQ. ID. NO. 38 A T A T T T G A G C A G G G G A A G A A A T C T G
 SEQ. ID. NO. 34 C C T G C C T C A C A G G T G G C C A T C T G C C
 SEQ. ID. NO. 30 G T G T G T A C C T T A C G G C G T C T T G G T T
 SEQ. ID. NO. 26 C C T G C C T C A C A G G T G G C C A T C T G C C

SEQ. ID. NO. 38 T C A C A G C G C C C A A G T T C A T T A G T C C
 SEQ. ID. NO. 34 T G G C A C T T A T C T C G G G C C A G C T G C T
 SEQ. ID. NO. 30 T G G G C A C T G C C T T C T C T G T C T G C T A
 SEQ. ID. NO. 26 T G G C A C T T A T C T C G G G C C A G C T G C T

SEQ. ID. NO. 38 A G C A T C T C A G C T G G T G A T C A C C T T C
 SEQ. ID. NO. 34 C A T C G T G G T C G C C T G G C T G G T G G T G
 SEQ. ID. NO. 30 C T C A G C C C T G C T C A C C A A G A C C A A C
 SEQ. ID. NO. 26 C A T C G T G G T C G C C T G G C T G G T G G T G

SEQ. ID. NO. 38 A G C C T C A T C T C C G T C C A G C T C C T T G
 SEQ. ID. NO. 34 G A G G C A C C G G G C A C A G G C A A G G A G A
 SEQ. ID. NO. 30 C G C A T T G C A C G C A T C T T C G G T G G G G
 SEQ. ID. NO. 26 G A G G C A C C G G G C A C A G G C A A G G A G A

SEQ. ID. NO. 38 G A G T G T T T G T C T G G T T T G T T G T G G A
 SEQ. ID. NO. 34 C A G C C C C C G A A C G G C G G G A G G T G G T
 SEQ. ID. NO. 30 C C C G G G A G G G T G C C C A G C G G C C A C G
 SEQ. ID. NO. 26 C A G C C C C C G A A C G G C G G G A G G T G G T

SEQ. ID. NO. 38 T C C C C C C C A C A T C A T C A T T G A C T A T
 SEQ. ID. NO. 34 G A C A C T G C G C T G C A A C C A C C G C G A T
 SEQ. ID. NO. 30 C T T C A T C A G T C C T G C C T C A C A G G T G
 SEQ. ID. NO. 26 G A C A C T G C G C T G C A A C C A C C G C G A T

SEQ. ID. NO. 38 G G A G A G C A G C G G A C A C T A G A T C C A G
 SEQ. ID. NO. 34 G C A A G T A T G T T G G G C T C G C T G G C C T
 SEQ. ID. NO. 30 G C C A T C T G C C T G G C A C T T A T C T C G G
 SEQ. ID. NO. 26 G C A A G T A T G T T G G G C T C G C T G G C C T

Figure 9k

SEQ. ID. NO. 38 A G A A G G C C A G G G G A G T G C T C A A G T G
 SEQ. ID. NO. 34 A C A A T G T G C T C C T C A T C G C G C T C T G
 SEQ. ID. NO. 30 G C C A G C T G C T C A T C G T G G T C G C C T G
 SEQ. ID. NO. 26 A C A A T G T G C T C C T C A T C G C G C T C T G

SEQ. ID. NO. 38 T G A C A T T T C T G A T C T C T C A C T C A T T
 SEQ. ID. NO. 34 C A C G C T T T A T G C C T T C A A G A C T C G C
 SEQ. ID. NO. 30 G C T G G T G G T G G A G G C A C C G G G C A C A
 SEQ. ID. NO. 26 C A C G C T T T A T G C C T T C A A T A C T C G C

SEQ. ID. NO. 38 T G T T C A C T T G G A T A C A G T A T C C T C T
 SEQ. ID. NO. 34 A A G T G C C C C G A A A A C T T C A A C G A G G
 SEQ. ID. NO. 30 G G C A A G G A G A C A G C C C C C G A A C G G C
 SEQ. ID. NO. 26 A A G T G C C C C G A A A A C T T C A A C G A G G

SEQ. ID. NO. 38 T G A T G G T C A C T T G T A C T G T T T A T G C
 SEQ. ID. NO. 34 C C A A G T T C A T T G G C T T C A C C A T G T A
 SEQ. ID. NO. 30 G G G A G G T G G T G A C A C T G C G C T G C A A
 SEQ. ID. NO. 26 C C A A G T T C A T T G G C T T C A C C A T G T A

SEQ. ID. NO. 38 C A T T A A A A C G A G A G G T G T C C C A G A G
 SEQ. ID. NO. 34 C A C C A C C T G C A T C A T C T G G C T G G C A
 SEQ. ID. NO. 30 C C A C C G C G A T G C A A G T A T G T T G G G C
 SEQ. ID. NO. 26 C A C C A C C T G C A T C A T C T G G C T G G C A

SEQ. ID. NO. 38 A C T T T C A A T G A A G C C A A A C C T A T T G
 SEQ. ID. NO. 34 T T C C T G C C C A T C T T C T A T G T C A C C T
 SEQ. ID. NO. 30 T C G C T G G C C T A C A A T G T G C T C C T C A
 SEQ. ID. NO. 26 T T G T T G C C C A T C T T C T A T G T C A C C T

SEQ. ID. NO. 38 G A T T T A C C A T G T A T A C C A C C T G C A T
 SEQ. ID. NO. 34 C C A G T G A C T A C C G G G T A C A G A C C A C
 SEQ. ID. NO. 30 T C G C G C T C T G C A C G C T T T A T G C C T T
 SEQ. ID. NO. 26 C C A G T G A C T A C C G G G T A C A G A C C A C

SEQ. ID. NO. 38 C A T T T G G T T A G C T T T C A T C C C C A T C
 SEQ. ID. NO. 34 C A C C A T G T G C G T G T C A G T C A G C C T C
 SEQ. ID. NO. 30 C A A T A C T C G C A A G T G C C C C G A A A A C
 SEQ. ID. NO. 26 C A C C A T G T G C G T G T C A G T C A G C C T C

Figure 91

SEQ. ID. NO. 38 T T T T T T G G T A C A G C C C A G T C A G C A G
 SEQ. ID. NO. 34 A G C G G C T C C G T G G T G C T T G G C T G C C
 SEQ. ID. NO. 30 T T C A A C G A G G C C A A G T T C A T T G G C T
 SEQ. ID. NO. 26 A G C G G C T C C G T G G T G C T T G G C T G C C

SEQ. ID. NO. 38 A A A A G A T G T A C A T C C A G A C A A C A A C
 SEQ. ID. NO. 34 T C T T T G C G C C C A A G C T G C A C A T C A T
 SEQ. ID. NO. 30 T C A C C A T G T A C A C C A C C T G C A T C A T
 SEQ. ID. NO. 26 T C T T T G C G C C C A A G C T G C A C A T C A T

SEQ. ID. NO. 38 A C T T A C T G T C T C C A T G A G T T T A A G T
 SEQ. ID. NO. 34 C C T C T T C C A G C C G C A G A A G A A C A C C
 SEQ. ID. NO. 30 C T G G C T G G C A T T G T T G C C C A T C T T C
 SEQ. ID. NO. 26 C C T C T T C C A G C C G C A G A A G A A C G T G

SEQ. ID. NO. 38 G C T T C A G T A T C T C T G G G C A T G C T C T
 SEQ. ID. NO. 34 A T C G A G G A G G T G C G T T G C A G C A C C G
 SEQ. ID. NO. 30 T A T G T C A C C T C C A G T G A C T A C C G G G
 SEQ. ID. NO. 26 G T T A G C C A C C G G G C A C C C A C C A G C C

SEQ. ID. NO. 38 A T A T G C C C A A G G T T T A T A T T A T A A T
 SEQ. ID. NO. 34 C A G C T C A C G C T T T C A A G G T G G C T G C
 SEQ. ID. NO. 30 T A C A G A C C A C C A C C A T G T G C G T G T C
 SEQ. ID. NO. 26 G C T T T G G C A G T G C T G C T G C C A G G G C

SEQ. ID. NO. 38 T T T T C A T C C A G A A C A G A A T A C C A T C
 SEQ. ID. NO. 34 C C G G G C C A C G C T G C G C C G C A G C A A C
 SEQ. ID. NO. 30 A G T C A G C C T C A G C G G C T C C G T G G T G
 SEQ. ID. NO. 26 C A G C T C C A G C C T T G G C C A A G G G T C T

SEQ. ID. NO. 38 G A G G A G G T G C G T T G C A G C A C C G C A G
 SEQ. ID. NO. 34 G T C T C C C G C A A G C G G T C C A G C A G C C
 SEQ. ID. NO. 30 C T T G G C T G C C T C T T T G C G C C C A A G C
 SEQ. ID. NO. 26 G G C T C C C A G T T T G T C C C C A C T G T T T

SEQ. ID. NO. 38 C T C A C G C T T T C A A G G T G G C T G C C C G
 SEQ. ID. NO. 34 T T G G A G G C T C C A C G G G A T C C A C C C C
 SEQ. ID. NO. 30 T G C A C A T C A T C C T C T T C C A G C C G C A
 SEQ. ID. NO. 26 G C A A T G G C C G T G A G G T G G T G G A C T C

Figure 9m

SEQ. ID. NO. 38 G G C C A C G C T G C G C C G C A G C A A C G T C
 SEQ. ID. NO. 34 C T C C T C C T C C A T C A G C A G C A A G A G C
 SEQ. ID. NO. 30 G A A G A A C G T G G T T A G C C A C C G G G C A
 SEQ. ID. NO. 26 G A C A A C G T C A T C G C T T

SEQ. ID. NO. 38 T C C C G C A A G C G G T C C A G C A G C C T T G
 SEQ. ID. NO. 34 A A C A G C G A A G A C C C A T T C C C A C A G C
 SEQ. ID. NO. 30 C C C A C C A G C C G C T T T G G C A G T G C T G
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G A G G C T C C A C G G G A T C C A C C C C C T C
 SEQ. ID. NO. 34 C C G A G A G G C A G A A G C A G C A G C A G C C
 SEQ. ID. NO. 30 C T G C C A G G G C C A G C T C C A G C C T T G G
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 C T C C T C C A T C A G C A G C A A G A G C A A C
 SEQ. ID. NO. 34 G C T G G C C C T A A C C C A G C A A G A G C A G
 SEQ. ID. NO. 30 C C A A G G G T C T G G C T C C C A G T T T G T C
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G C G A A G A C C C A T T C C C A C A G C C C G
 SEQ. ID. NO. 34 C A G C A G C A G C C C C T G A C C C T C C C A C
 SEQ. ID. NO. 30 C C C A C T G T T T G C A A T G G C C G T G A G G
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G A G G C A G A A G C A G C A G C A G C C G C T
 SEQ. ID. NO. 34 A G C A G C A A C G A T C T C A G C A G C A G C C
 SEQ. ID. NO. 30 T G G T G G A C T C G A C A A C G T C A T C G C T
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G G C C C T A A C C C A G C A A G A G C A G C A G
 SEQ. ID. NO. 34 C A G A T G C A A G C A G A A G G T C A T C T T T
 SEQ. ID. NO. 30 T
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A G C A G C C C C T G A C C C T C C C A C A G C
 SEQ. ID. NO. 34 G G C A G C G G C A C G G T C A C C T T C T C A C
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

Figure 9n

SEQ. ID. NO. 38 A G C A A C G A T C T C A G C A G C A G C C C A G
 SEQ. ID. NO. 34 T G A G C T T T G A T G A G C C T C A G A A G A A
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 A T G C A A G C A G A A G G T C A T C T T T G G C
 SEQ. ID. NO. 34 C G C C A T G G C C C A C G G G A A T T C T A C G
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G C G G C A C G G T C A C C T T C T C A C T G A
 SEQ. ID. NO. 34 C A C C A G A A C T C C C T G G A G G C C C A G A
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C T T T G A T G A G C C T C A G A A G A A C G C
 SEQ. ID. NO. 34 A A A G C A G C G A T A C G C T G A C C C G A C A
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A T G G C C C A C G G G A A T T C T A C G C A C
 SEQ. ID. NO. 34 C C A G C C A T T A C T C C C G C T G C A G T G C
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A G A A C T C C C T G G A G G C C C A G A A A A
 SEQ. ID. NO. 34 G G G G A A A C G G A C T T A G A T C T G A C C G
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C A G C G A T A C G C T G A C C C G A C A C C A
 SEQ. ID. NO. 34 T C C A G G A A A C A G G T C T G C A A G G A C C
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C C A T T A C T C C C G C T G C A G T G C G G G
 SEQ. ID. NO. 34 T G T G G G T G G A G A C C A G C G G C C A G A G
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

Figure 9o

SEQ. ID. NO. 38 G A A A C G G A C T T A G A T C T G A C C G T C C
SEQ. ID. NO. 34 G T G G A G G A C C C T G A A G A G T T G T C C C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G G A A A C A G G T C T G C A A G G A C C T G T
SEQ. ID. NO. 34 C A G C A C T T G T A G T G T C C A G T T C A C A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G G G T G G A G A C C A G C G G C C A G A G G T G
SEQ. ID. NO. 34 G A G C T T T G T C A T C A G T G G T G G A G G C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G A G G A C C C T G A A G A G T T G T C C C C A G
SEQ. ID. NO. 34 A G C A C T G T T A C A G A A A A C G T A G T G A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A C T T G T A G T G T C C A G T T C A C A G A G
SEQ. ID. NO. 34 A T T C A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C T T T G T C A T C A G T G G T G G A G G C A G C
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A C T G T T A C A G A A A A C G T A G T G A A T T
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

Figure 9p

ClustalW Formatted Alignments

SEQ. ID. NO. 39 M V C E G K R S A S C P C F F L L T A K F Y W I L
 SEQ. ID. NO. 35 M G S L L A L P A L L L L W G A V A E G P A K K V
 SEQ. ID. NO. 31 M A F Y S C C W V L L A L T W H T S A Y G P D Q R
 SEQ. ID. NO. 27 M G S L L A L L A L L P L W G A V A E G P A K K V

SEQ. ID. NO. 39 T M M Q R T H S Q E Y A H S I R V D G D I I L G G
 SEQ. ID. NO. 35 L T L E G D L V L G G L F P V H Q K G G P A E D C
 SEQ. ID. NO. 31 A Q K K G D I I L G G L F P I H F G V A A K D Q D
 SEQ. ID. NO. 27 L T L E G D L V L G G L F P V H Q K G G P A E D C

SEQ. ID. NO. 39 L F P V H A K G E R G V P C G E L K K E K G I H R
 SEQ. ID. NO. 35 G P V N E H R G I Q R L E A M L F A L D R I N R D
 SEQ. ID. NO. 31 L K S R P E S V E C I R Y N F R G F R W L Q A M I
 SEQ. ID. NO. 27 G P V N E H R G I Q R L E A M L F A L D R I N R D

SEQ. ID. NO. 39 L E A M L Y A I D Q I N K D P D L L S N I T L G V
 SEQ. ID. NO. 35 P H L L P G V R L G A H I L D S C S K D T H A L E
 SEQ. ID. NO. 31 F A I E E I N S S P A L L P N L T L G Y R I F D T
 SEQ. ID. NO. 27 P H L L P G V R L G A H I L D S C S K D T H A L E

SEQ. ID. NO. 39 R I L D T C S R D T Y A L E Q S L T F V Q A L I E
 SEQ. ID. NO. 35 Q A L D F V R A S L S R G A D G S R H I C P D G S
 SEQ. ID. NO. 31 C N T V S K A L E A T L S F V A Q N K I D S L N L
 SEQ. ID. NO. 27 Q A L D F V R A S L S R G A D G S R H I C P D G S

SEQ. ID. NO. 39 K D A S D V K C A N G D P P I F T K P D K I S G V
 SEQ. ID. NO. 35 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
 SEQ. ID. NO. 31 D E F C N C S E H I P S T I A V V G A T G S G V S
 SEQ. ID. NO. 27 Y A T H G D A P T A I T G V I G G S Y S D V S I Q

SEQ. ID. NO. 39 I G A A A S S V S I M V A N I L R L F K I P Q I S
 SEQ. ID. NO. 35 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
 SEQ. ID. NO. 31 T A V A N L L G L F Y I P Q V S Y A S S S R L L S
 SEQ. ID. NO. 27 V A N L L R L F Q I P Q I S Y A S T S A K L S D K

SEQ. ID. NO. 39 Y A S T A P E L S D N T R Y D F F S R V V P P D S
 SEQ. ID. NO. 35 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
 SEQ. ID. NO. 31 N K N Q F K S F L R T I P N D E H Q A T A M A D I
 SEQ. ID. NO. 27 S R Y D Y F A R T V P P D F F Q A K A M A E I L R

Figure 10a

SEQ. ID. NO. 39 YQAQAMVDIVTALGWNYVSTLASSEG
 SEQ. ID. NO. 35 FFNWTYVSTVASEGDYGETGIEAFE
 SEQ. ID. NO. 31 IEYFRWNWVGTTAADDYGRPGIEK
 SEQ. ID. NO. 27 FFNWTYVSTEASEGDYGETGIEAFE

SEQ. ID. NO. 39 NYGESGVEAFTQISREIGGVCI AQ S
 SEQ. ID. NO. 35 LEARARNICVATSEKVGGRAMSRAAF
 SEQ. ID. NO. 31 FREEAEERDICI DFSELISQYSDEE
 SEQ. ID. NO. 27 LEARARNICVATSEKVGGRAMSRAAF

SEQ. ID. NO. 39 QKIPREPRPGEFEKI IKRLLET PNA
 SEQ. ID. NO. 35 EGVVRALLQKPSARVAVL FTRSEDA
 SEQ. ID. NO. 31 EI QHVVEVI QNSTAKVI VVFS SGP D
 SEQ. ID. NO. 27 EGVVRALLQKPSARVAVL FTRSEDA

SEQ. ID. NO. 39 RAVIMFANEDDIRRI LEAAKKLNQ S
 SEQ. ID. NO. 35 REL LAASQRLNASFTWV ASDGWGAL
 SEQ. ID. NO. 31 LEPLIKEIVRRNITGKIWLASEAWA
 SEQ. ID. NO. 27 REL LAASQRLNASFTWV ASDGWGAL

SEQ. ID. NO. 39 GHFLWIGSDSWGSKIAPVYQQEEIA
 SEQ. ID. NO. 35 ESVVAGSEGAAEGAITIELASYPIS
 SEQ. ID. NO. 31 SSSLIAMPPQYFHVVG GTIGFALKAG
 SEQ. ID. NO. 27 ESVVAGSEGAAEGAITIELASYPIS

SEQ. ID. NO. 39 EGAVTILPKRASIDGFDRYFRSRTL
 SEQ. ID. NO. 35 DFASYFQSLDPWNN SRNPWFREFWE
 SEQ. ID. NO. 31 QIPGFREFLKKVHPRKSVHNGFAKE
 SEQ. ID. NO. 27 DFASYFQSLDPWNN SRNPWFREFWE

SEQ. ID. NO. 39 ANNRRNVWF AEFW EENFGCKLGSHG
 SEQ. ID. NO. 35 QRFRC SFRQRDCAAHSLRAVPFEQE
 SEQ. ID. NO. 31 FWEETFNCHLQEGAKGPLPVD TFLR
 SEQ. ID. NO. 27 QRFRC SFRQRDCAAHSLRAVPFEQE

SEQ. ID. NO. 39 KRN SHIKKCTGLERI ARDSSYEQEG
 SEQ. ID. NO. 35 SKIMFVVNAVYAMAHALHNMHRA LC
 SEQ. ID. NO. 31 GHEESGDRFSNSSTA FRPLCTGDEN
 SEQ. ID. NO. 27 SKIMFVVNAVYAMAHALHNMHRA LC

Figure 10b

SEQ. ID. NO. 39 K V Q F V I D A V Y S M A Y A L H N M H K D L C P
 SEQ. ID. NO. 35 P N T T R L C D A M R P V N G R R L Y K D F V L N
 SEQ. ID. NO. 31 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y
 SEQ. ID. NO. 27 P N T T R L C D A M R P V N G R R L Y K D F V L N

SEQ. ID. NO. 39 G Y I G L C P R M S T I D G K E L L G Y I R A V N
 SEQ. ID. NO. 35 V K F D A P F R P A D T H N E V R F D R F G D G I
 SEQ. ID. NO. 31 S I A H A L Q D I Y T C L P G R G L F T N G S C A
 SEQ. ID. NO. 27 V K F D A P F R P A D T H N E V R F D R F G D G I

SEQ. ID. NO. 39 F N G S A G T P V T F N E N G D A P G R Y D I F Q
 SEQ. ID. NO. 35 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
 SEQ. ID. NO. 31 D I K K V E A W Q V L K H L R H L N F T N N M G E
 SEQ. ID. NO. 27 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A

SEQ. ID. NO. 39 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E
 SEQ. ID. NO. 35 E G L T L D T S L I P W A S P S A G P L P A S R C
 SEQ. ID. NO. 31 Q V T F D E C G D L V G N Y S I I N W H L S P E D
 SEQ. ID. NO. 27 E G L T L D T S L I P W A S P S A G P L A A S R C

SEQ. ID. NO. 39 D M Q W A H R E H T H P A S V C S L P C K P G E R
 SEQ. ID. NO. 35 S E P C L Q N E V K S V Q P G E V C C W L C I P C
 SEQ. ID. NO. 31 G S I V F K E V G Y Y N V Y A K K G E R L F I N E
 SEQ. ID. NO. 27 S E P C L Q N E V K S V Q P G E V C C W L C I P C

SEQ. ID. NO. 39 K K T V K G V P C C W H C E R C E G Y N Y Q V D E
 SEQ. ID. NO. 35 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
 SEQ. ID. NO. 31 E K I L W S G F S R E V P F S N C S R D C L A G T
 SEQ. ID. NO. 27 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L

SEQ. ID. NO. 39 L S C E L C P L D Q R P N M N R T G C Q L I P I I
 SEQ. ID. NO. 35 T G C F E L P Q E Y I R W G D A W A V G P V T I A
 SEQ. ID. NO. 31 R K G I I E G E P T C C F E C V E C P D G E Y S D
 SEQ. ID. NO. 27 T G C F E L P Q E Y I R W G D A W A V G P V T I A

SEQ. ID. NO. 39 K L E W H S P W A V V P V F V A I L G I I A T T F
 SEQ. ID. NO. 35 C L G A L A T L F V L G V F V R H N A T P V V K A
 SEQ. ID. NO. 31 E T D A S A C N K C P D D F W S N E N H T S C F E
 SEQ. ID. NO. 27 C L G A L A T L F V L G V F V R H N A T P V V K A

Figure 10c

SEQ. ID. NO. 39 V I V T F V R Y N D T P I V R A S G R E L S Y V L
 SEQ. ID. NO. 35 S G R E L C Y I L L G G V F L C Y C M T F I F I A
 SEQ. ID. NO. 31 L P Q E Y I R W G D A W A V G P V T I A C L G A L
 SEQ. ID. NO. 27 S G R E L C Y I L L G G V F L C Y C M T F I F I A

SEQ. ID. NO. 39 L T G I F L C Y S I T F L M I A A P D T I I C S F
 SEQ. ID. NO. 35 K P S T A V C T L R R L G L G T A F S V C Y S A L
 SEQ. ID. NO. 31 A T L F V L G V F V R H N A T P V V K A S G R E L
 SEQ. ID. NO. 27 K P S T A V C T L R R L G L G T A F S V C Y S A L

SEQ. ID. NO. 39 R R V F L G L G M C F S Y A A L L T K T N R I H R
 SEQ. ID. NO. 35 L T K T N R I A R I F G G A R E G A Q R P R F I S
 SEQ. ID. NO. 31 C Y I L L G G V F L C Y C M T F I F I A K P S T A
 SEQ. ID. NO. 27 L T K T N R I A R I F G G A R E G A Q R P R F I S

SEQ. ID. NO. 39 I F E Q G K K S V T A P K F I S P A S Q L V I T F
 SEQ. ID. NO. 35 P A S Q V A I C L A L I S G Q L L I V V A W L V V
 SEQ. ID. NO. 31 V C T L R R L G L G T A F S V C Y S A L L T K T N
 SEQ. ID. NO. 27 P A S Q V A I C L A L I S G Q L L I V V A W L V V

SEQ. ID. NO. 39 S L I S V Q L L G V F V W F V V D P P H I I I D Y
 SEQ. ID. NO. 35 E A P G T G K E T A P E R R E V V T L R C N H R D
 SEQ. ID. NO. 31 R I A R I F G G A R E G A Q R P R F I S P A S Q V
 SEQ. ID. NO. 27 E A P G T G K E T A P E R R E V V T L R C N H R D

SEQ. ID. NO. 39 G E Q R T L D P E K A R G V L K C D I S D L S L I
 SEQ. ID. NO. 35 A S M L G S L A Y N V L L I A L C T L Y A F K T R
 SEQ. ID. NO. 31 A I C L A L I S G Q L L I V V A W L V V E A P G T
 SEQ. ID. NO. 27 A S M L G S L A Y N V L L I A L C T L Y A F N T R

SEQ. ID. NO. 39 C S L G Y S I L L M V T C T V Y A I K T R G V P E
 SEQ. ID. NO. 35 K C P E N F N E A K F I G F T M Y T T C I I W L A
 SEQ. ID. NO. 31 G K E T A P E R R E V V T L R C N H R D A S M L G
 SEQ. ID. NO. 27 K C P E N F N E A K F I G F T M Y T T C I I W L A

SEQ. ID. NO. 39 T F N E A K P I G F T M Y T T C I I W L A F I P I
 SEQ. ID. NO. 35 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
 SEQ. ID. NO. 31 S L A Y N V L L I A L C T L Y A F N T R K C P E N
 SEQ. ID. NO. 27 L L P I F Y V T S S D Y R V Q T T T M C V S V S L

Figure 10d

SEQ. ID. NO. 39 F F G T A Q S A E K M Y I Q T T T L T V S M S L S
 SEQ. ID. NO. 35 S G S V V L G C L F A P K L H I I L F Q P Q K N T
 SEQ. ID. NO. 31 F N E A K F I G F T M Y T T C I I W L A L L P I F
 SEQ. ID. NO. 27 S G S V V L G C L F A P K L H I I L F Q P Q K N

SEQ. ID. NO. 39 A S V S L G M L Y M P K V Y I I I F H P E Q N T I
 SEQ. ID. NO. 35 I E E V R C S T A A H A F K V A A R A T L R R S N
 SEQ. ID. NO. 31 Y V T S S D Y R V Q T T T M C V S V S L S G S V V
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 E E V R C S T A A H A F K V A A R A T L R R S N V
 SEQ. ID. NO. 35 V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 31 L G C L F A P K L H I I L F Q P Q K N V V S H R A
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 S R K R S S S L G G S T G S T P S S S I S S K S N
 SEQ. ID. NO. 35 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
 SEQ. ID. NO. 31 P T S R F G S A A A R A S S S L G Q G S G S Q F V
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q
 SEQ. ID. NO. 35 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
 SEQ. ID. NO. 31 P T V C N G R E V V D S T T S S L
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F G
 SEQ. ID. NO. 35 G S G T V T F S L S F D E P Q K N A M A H G N S T
 SEQ. ID. NO. 31
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 S G T V T F S L S F D E P Q K N A M A H G N S T H
 SEQ. ID. NO. 35 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
 SEQ. ID. NO. 31
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 Q N S L E A Q K S S D T L T R H Q P L L P L Q C G
 SEQ. ID. NO. 35 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
 SEQ. ID. NO. 31
 SEQ. ID. NO. 27

Figure 10e

SEQ. ID. NO. 39 E T D L D L T V Q E T G L Q G P V G G D Q R P E V
SEQ. ID. NO. 35 V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 31
SEQ. ID. NO. 27

SEQ. ID. NO. 39 E D P E E L S P A L V V S S S Q S F V I S G G G S
SEQ. ID. NO. 35 S T V T E N V V N S
SEQ. ID. NO. 31
SEQ. ID. NO. 27

SEQ. ID. NO. 39 T V T E N V V N S
SEQ. ID. NO. 35
SEQ. ID. NO. 31
SEQ. ID. NO. 27

ClustalW Formatted Alignments

SEQ. ID. NO. 40 A T G G T A T G C G A G G G A A A G C G A T C A G
 SEQ. ID. NO. 46 A T G G G A T C G C T G C T T G C G C T C C C G G
 SEQ. ID. NO. 36 A T G G G A T C G C T G C T T G C G C T C C C G G
 SEQ. ID. NO. 32 A T G G C A T T T T A T A G C T G C T G C T G G G

SEQ. ID. NO. 40 C C T C T T G C C C T T G T T T C T T C C T C T T
 SEQ. ID. NO. 46 C A C T G C T G C T G C T G T G G G G T G C T G T
 SEQ. ID. NO. 36 C A C T G C T G C T G C T G T G G G G T G C T G T
 SEQ. ID. NO. 32 T C C T C T T G G C A C T C A C C T G G C A C A C

SEQ. ID. NO. 40 G A C C G C C A A G T T C T A C T G G A T C C T C
 SEQ. ID. NO. 46 G G C T G A G G G C C C A G C C A A G A A G G T G
 SEQ. ID. NO. 36 G G C T G A G G G C C C A G C C A A G A A G G T G
 SEQ. ID. NO. 32 C T C T G C C T A C G G G C C A G A C C A G C G A

SEQ. ID. NO. 40 A C A A T G A T G C A A A G A A C T C A C A G C C
 SEQ. ID. NO. 46 C T G A C C C T G G A G G G A G A C T T G G T G C
 SEQ. ID. NO. 36 C T G A C C C T G G A G G G A G A C T T G G T G C
 SEQ. ID. NO. 32 G C C C A A A A G A A G G G G G A C A T T A T C C

SEQ. ID. NO. 40 A G G A G T A T G C C C A T T C C A T A C G G G T
 SEQ. ID. NO. 46 T G G G T G G G C T G T T C C C A G T G C A C C A
 SEQ. ID. NO. 36 T G G G T G G G C T G T T C C C A G T G C A C C A
 SEQ. ID. NO. 32 T T G G G G G G C T C T T T C C T A T T C A T T T

SEQ. ID. NO. 40 G G A T G G G G A C A T T A T T T T G G G G G G T
 SEQ. ID. NO. 46 G A A G G G C G G C C C A G C A G A G G A C T G T
 SEQ. ID. NO. 36 G A A G G G C G G C C C A G C A G A G G A C T G T
 SEQ. ID. NO. 32 T G G A G T A G C A G C T A A A G A T C A A G A T

SEQ. ID. NO. 40 C T C T T C C C T G T C C A C G C A A A G G G A G
 SEQ. ID. NO. 46 G G T C C T G T C A A T G A G C A C C G T G G C A
 SEQ. ID. NO. 36 G G T C C T G T C A A T G A G C A C C G T G G C A
 SEQ. ID. NO. 32 C T C A A A T C A A G G C C G G A G T C T G T G G

SEQ. ID. NO. 40 A G A G A G G G G T G C C T T G T G G G G A G C T
 SEQ. ID. NO. 46 T C C A G C G C C T G G A G G C C A T G C T T T T
 SEQ. ID. NO. 36 T C C A G C G C C T G G A G G C C A T G C T T T T
 SEQ. ID. NO. 32 A A T G T A T C A G G T A T A A T T T C C G T G G

Figure 11a

SEQ. ID. NO. 40 G A A G A A G G A A A A G G G G A T T C A C A G A
 SEQ. ID. NO. 46 T G C A C T G G A C C G C A T C A A C C G T G A C
 SEQ. ID. NO. 36 T G C A C T G G A C C G C A T C A A C C G T G A C
 SEQ. ID. NO. 32 G T T T C G C T G G T T A C A G G C T A T G A T A

SEQ. ID. NO. 40 C T G G A G G C C A T G C T T T A T G C A A T T G
 SEQ. ID. NO. 46 C C G C A C C T G C T G C C T G G C G T G C G C C
 SEQ. ID. NO. 36 C C G C A C C T G C T G C C T G G C G T G C G C C
 SEQ. ID. NO. 32 T T T G C C A T A G A G G A G A T A A A C A G C A

SEQ. ID. NO. 40 A C C A G A T T A A C A A G G A C C C T G A T C T
 SEQ. ID. NO. 46 T G G G T G C A C A C A T C C T C G A C A G T T G
 SEQ. ID. NO. 36 T G G G T G C A C A C A T C C T C G A C A G T T G
 SEQ. ID. NO. 32 G C C C A G C C C T T C T T C C C A A C T T G A C

SEQ. ID. NO. 40 C C T T T C C A A C A T C A C T C T G G G T G T C
 SEQ. ID. NO. 46 C T C C A A G G A C A C A C A T G C G C T G G A G
 SEQ. ID. NO. 36 C T C C A A G G A C A C A C A T G C G C T G G A G
 SEQ. ID. NO. 32 G C T G G G A T A C A G G A T A T T T G A C A C T

SEQ. ID. NO. 40 C G C A T C C T C G A C A C G T G C T C T A G G G
 SEQ. ID. NO. 46 C A G G C A C T G G A C T T T G T G C G T G C C T
 SEQ. ID. NO. 36 C A G G C A C T G G A C T T T G T G C G T G C C T
 SEQ. ID. NO. 32 T G C A A C A C C G T T T C T A A G G C C T T G G

SEQ. ID. NO. 40 A C A C C T A T G C T T T G G A G C A G T C T C T
 SEQ. ID. NO. 46 C A C T C A G C C G T G G T G C T G A T G G C T C
 SEQ. ID. NO. 36 C A C T C A G C C G T G G T G C T G A T G G C T C
 SEQ. ID. NO. 32 A A G C C A C C C T G A G T T T T G T T G C T C A

SEQ. ID. NO. 40 A A C A T T C G T G C A G G C A T T A A T A G A G
 SEQ. ID. NO. 46 A C G C C A C A T C T G C C C C G A C G G C T C T
 SEQ. ID. NO. 36 A C G C C A C A T C T G C C C C G A C G G C T C T
 SEQ. ID. NO. 32 A A A C A A A A T T G A T T C T T T G A A C C T T

SEQ. ID. NO. 40 A A A G A T G C T T C G G A T G T G A A G T G T G
 SEQ. ID. NO. 46 T A T G C G A C C C A T G G T G A T G C T C C C A
 SEQ. ID. NO. 36 T A T G C G A C C C A T G G T G A T G C T C C C A
 SEQ. ID. NO. 32 G A T G A G T T C T G C A A C T G C T C A G A G C

Figure 11b

SEQ. ID. NO. 40 C T A A T G G A G A T C C A C C C A T T T T C A C
 SEQ. ID. NO. 46 C T G C C A T C A C T G G T G T T A T T G G C G G
 SEQ. ID. NO. 36 C T G C C A T C A C T G G T G T T A T T G G C G G
 SEQ. ID. NO. 32 A C A T T C C C T C T A C G A T T G C T G T G G T

SEQ. ID. NO. 40 C A A G C C C G A C A A G A T T T C T G G C G T C
 SEQ. ID. NO. 46 T T C C T A C A G T G A T G T C T C C A T C C A G
 SEQ. ID. NO. 36 T T C C T A C A G T G A T G T C T C C A T C C A G
 SEQ. ID. NO. 32 G G G A G C A A C T G G C T C A G G C G T C T C C

SEQ. ID. NO. 40 A T A G G T G C T G C A G C A A G C T C C G T G T
 SEQ. ID. NO. 46 G T G G C C A A C C T C T T G A G G C T A T T T C
 SEQ. ID. NO. 36 G T G G C C A A C C T C T T G A G G C T A T T T C
 SEQ. ID. NO. 32 A C G G C A G T G G C A A A T C T G C T G G G G C

SEQ. ID. NO. 40 C C A T C A T G G T T G C T A A C A T T T T A A G
 SEQ. ID. NO. 46 A G A T C C C A C A G A T T A G C T A C G C C T C
 SEQ. ID. NO. 36 A G A T C C C A C A G A T T A G C T A C G C C T C
 SEQ. ID. NO. 32 T C T T C T A C A T T C C C C A G G T C A G T T A

SEQ. ID. NO. 40 A C T T T T T A A G A T A C C T C A A A T C A G C
 SEQ. ID. NO. 46 T A C C A G T G C C A A G C T G A G T G A C A A G
 SEQ. ID. NO. 36 T A C C A G T G C C A A G C T G A G T G A C A A G
 SEQ. ID. NO. 32 T G C C T C C T C C A G C A G A C T C C T C A G C

SEQ. ID. NO. 40 T A T G C A T C C A C A G C C C C A G A G C T A A
 SEQ. ID. NO. 46 T C C C G C T A T G A C T A C T T T G C C C G C A
 SEQ. ID. NO. 36 T C C C G C T A T G A C T A C T T T G C C C G C A
 SEQ. ID. NO. 32 A A C A A G A A T C A A T T C A A G T C T T T C C

SEQ. ID. NO. 40 G T G A T A A C A C C A G G T A T G A C T T T T T
 SEQ. ID. NO. 46 C A G T G C C T C C T G A C T T C T T C C A A G C
 SEQ. ID. NO. 36 C A G T G C C T C C T G A C T T C T T C C A A G C
 SEQ. ID. NO. 32 T C C G A A C C A T C C C C A A T G A T G A G C A

SEQ. ID. NO. 40 C T C T C G A G T G G T T C C G C C T G A C T C C
 SEQ. ID. NO. 46 C A A G G C C A T G G C T G A G A T T C T C C G C
 SEQ. ID. NO. 36 C A A G G C C A T G G C T G A G A T T C T C C G C
 SEQ. ID. NO. 32 C C A G G C C A C T G C C A T G G C A G A C A T C

Figure 11c

SEQ. ID. NO. 40 T A C C A A G C C C A A G C C A T G G T G G A C A
 SEQ. ID. NO. 46 T T C T T C A A C T G G A C C T A T G T G T C C A
 SEQ. ID. NO. 36 T T C T T C A A C T G G A C C T A T G T G T C C A
 SEQ. ID. NO. 32 A T C G A G T A T T T C C G C T G G A A C T G G G

SEQ. ID. NO. 40 T C G T G A C A G C A C T G G G A T G G A A T T A
 SEQ. ID. NO. 46 C T G T G G C G T C T G A G G G C G A C T A T G G
 SEQ. ID. NO. 36 C T G T G G C G T C T G A G G G C G A C T A T G G
 SEQ. ID. NO. 32 T G G G C A C A A T T G C A G C T G A T G A C G A

SEQ. ID. NO. 40 T G T T T C G A C A C T G G C T T C T G A G G G G
 SEQ. ID. NO. 46 C G A G A C A G G C A T T G A G G C C T T T G A G
 SEQ. ID. NO. 36 C G A G A C A G G C A T T G A G G C C T T T G A G
 SEQ. ID. NO. 32 C T A T G G G C G G C C G G G G A T T G A G A A A

SEQ. ID. NO. 40 A A C T A T G G T G A G A G C G G T G T G G A G G
 SEQ. ID. NO. 46 C T A G A G G C T C G T G C C C G C A A C A T C T
 SEQ. ID. NO. 36 C T A G A G G C T C G T G C C C G C A A C A T C T
 SEQ. ID. NO. 32 T T C C G A G A G G A A G C T G A G G A A A G G G

SEQ. ID. NO. 40 C C T T C A C C C A G A T C T C G A G G G A G A T
 SEQ. ID. NO. 46 G T G T G G C C A C C T C G G A G A A A G T G G G
 SEQ. ID. NO. 36 G T G T G G C C A C C T C G G A G A A A G T G G G
 SEQ. ID. NO. 32 A T A T C T G C A T C G A C T T C A G T G A A C T

SEQ. ID. NO. 40 T G G T G G T G T T T G C A T T G C T C A G T C A
 SEQ. ID. NO. 46 C C G T G C C A T G A G C C G C G C G G C C T T T
 SEQ. ID. NO. 36 C C G T G C C A T G A G C C G C G C G G C C T T T
 SEQ. ID. NO. 32 C A T C T C C C A G T A C T C T G A T G A G G A A

SEQ. ID. NO. 40 C A G A A A A T C C C A C G T G A A C C A A G A C
 SEQ. ID. NO. 46 G A G G G T G T G G T G C G A G C C C T G C T G C
 SEQ. ID. NO. 36 G A G G G T G T G G T G C G A G C C C T G C T G C
 SEQ. ID. NO. 32 G A G A T C C A G C A T G T G G T A G A G G T G A

SEQ. ID. NO. 40 C T G G A G A A T T T G A A A A A A T T A T C A A
 SEQ. ID. NO. 46 A G A A G C C C A G T G C C C G C G T G G C T G T
 SEQ. ID. NO. 36 A G A A G C C C A G T G C C C G C G T G G C T G T
 SEQ. ID. NO. 32 T T C A A A A T T C C A C G G C C A A A G T C A T

Figure 11d

SEQ. ID. NO. 40 A C G C C T G C T A G A A A C A C C T A A T G C T
 SEQ. ID. NO. 46 C C T G T T C A C C C G T T C T G A G G A T G C C
 SEQ. ID. NO. 36 C C T G T T C A C C C G T T C T G A G G A T G C C
 SEQ. ID. NO. 32 C G T G G T T T T C T C A G T G G C C C A G A T

SEQ. ID. NO. 40 C G A G C A G T G A T T A T G T T T G C C A A T G
 SEQ. ID. NO. 46 C G G G A G C T G C T T G C T G C C A G C C A G C
 SEQ. ID. NO. 36 C G G G A G C T G C T T G C T G C C A G C C A G C
 SEQ. ID. NO. 32 C T T G A G C C C C T C A T C A A G G A G A T T G

SEQ. ID. NO. 40 A G G A T G A C A T C A G G A G G A T A T T G G A
 SEQ. ID. NO. 46 G C C T C A A T G C C A G C T T C A C C T G G G T
 SEQ. ID. NO. 36 G C C T C A A T G C C A G C T T C A C C T G G G T
 SEQ. ID. NO. 32 T C C G G C G C A A T A T C A C G G G C A A G A T

SEQ. ID. NO. 40 A G C A G C A A A A A A A C T A A A C C A A A G T
 SEQ. ID. NO. 46 G G C C A G T G A T G G T T G G G G G G C C C T G
 SEQ. ID. NO. 36 G G C C A G T G A T G G T T G G G G G G C C C T G
 SEQ. ID. NO. 32 C T G G C T G G C C A G C G A G G C C T G G G C C

SEQ. ID. NO. 40 G G G C A T T T T C T C T G G A T T G G C T C A G
 SEQ. ID. NO. 46 G A G A G T G T G G T G G C A G G C A G T G A G G
 SEQ. ID. NO. 36 G A G A G T G T G G T G G C A G G C A G T G A G G
 SEQ. ID. NO. 32 A G C T C C T C C C T G A T C G C C A T G C C T C

SEQ. ID. NO. 40 A T A G T T G G G G A T C C A A A A T A G C A C C
 SEQ. ID. NO. 46 G G G C T G C T G A G G G T G C T A T C A C C A T
 SEQ. ID. NO. 36 G G G C T G C T G A G G G T G C T A T C A C C A T
 SEQ. ID. NO. 32 A G T A C T T C C A C G T G G T T G G C G G C A C

SEQ. ID. NO. 40 T G T C T A T C A G C A A G A G G A G A T T G C A
 SEQ. ID. NO. 46 C G A G C T G G C C T C C T A C C C C A T C A G T
 SEQ. ID. NO. 36 C G A G C T G G C C T C C T A C C C C A T C A G T
 SEQ. ID. NO. 32 C A T T G G A T T C G C T C T G A A G G C T G G G

SEQ. ID. NO. 40 G A A G G G G C T G T G A C A A T T T T G C C C A
 SEQ. ID. NO. 46 G A C T T T G C C T C C T A C T T C C A G A G C C
 SEQ. ID. NO. 36 G A C T T T G C C T C C T A C T T C C A G A G C C
 SEQ. ID. NO. 32 C A G A T C C C A G G C T T C C G G G A A T T C C

Figure 11e

SEQ. ID. NO. 40 A A C G A G C A T C A A T T G A T G G A T T T G A
 SEQ. ID. NO. 46 T G G A C C C T T G G A A C A A C A G C C G G A A
 SEQ. ID. NO. 36 T G G A C C C T T G G A A C A A C A G C C G G A A
 SEQ. ID. NO. 32 T G A A G A A G G T C C A T C C C A G G A A G T C

SEQ. ID. NO. 40 T C G A T A C T T T A G A A G C C G A A C T C T T
 SEQ. ID. NO. 46 C C C C T G G T T C C G T G A A T T C T G G G A G
 SEQ. ID. NO. 36 C C C C T G G T T C C G T G A A T T C T G G G A G
 SEQ. ID. NO. 32 T G T C C A C A A T G G T T T T G C C A A G G A G

SEQ. ID. NO. 40 G C C A A T A A T C G A A G A A A T G T G T G G T
 SEQ. ID. NO. 46 C A G A G G T T C C G C T G C A G C T T C C G G C
 SEQ. ID. NO. 36 C A G A G G T T C C G C T G C A G C T T C C G G C
 SEQ. ID. NO. 32 T T T T G G G A A G A A A C A T T T A A C T G C C

SEQ. ID. NO. 40 T T G C A G A A T T C T G G G A G G A G A A T T T
 SEQ. ID. NO. 46 A G C G A G A C T G C G C A G C C C A C T C T C T
 SEQ. ID. NO. 36 A G C G A G A C T G C G C A G C C C A C T C T C T
 SEQ. ID. NO. 32 A C C T C C A A G A A G G T G C A A A A G G A C C

SEQ. ID. NO. 40 T G G C T G C A A G T T A G G A T C A C A T G G G
 SEQ. ID. NO. 46 C C G G G C T G T G C C C T T T G A G C A G G A G
 SEQ. ID. NO. 36 C C G G G C T G T G C C C T T T G A G C A G G A G
 SEQ. ID. NO. 32 T T T A C C T G T G G A C A C C T T T C T G A G A

SEQ. ID. NO. 40 A A A A G G A A C A G T C A T A T A A A G A A A T
 SEQ. ID. NO. 46 T C C A A G A T C A T G T T T G T G G T C A A T G
 SEQ. ID. NO. 36 T C C A A G A T C A T G T T T G T G G T C A A T G
 SEQ. ID. NO. 32 G G T C A C G A A G A A A G T G G C G A C A G G T

SEQ. ID. NO. 40 G C A C A G G G C T G G A G C G A A T T G C T C G
 SEQ. ID. NO. 46 C A G T G T A C G C C A T G G C C C A T G C G C T
 SEQ. ID. NO. 36 C A G T G T A C G C C A T G G C C C A T G C G C T
 SEQ. ID. NO. 32 T T A G C A A C A G C T C G A C A G C C T T C C G

SEQ. ID. NO. 40 G G A T T C A T C T T A T G A A C A G G A A G G A
 SEQ. ID. NO. 46 C C A C A A C A T G C A C C G T G C C C T C T G C
 SEQ. ID. NO. 36 C C A C A A C A T G C A C C G T G C C C T C T G C
 SEQ. ID. NO. 32 A C C C C T C T G T A C A G G G G A T G A G A A C

Figure 11f

SEQ. ID. NO. 40 A A G G T C C A A T T T G T A A T T G A T G C T G
 SEQ. ID. NO. 46 C C C A A C A C C A C C C G G C T C T G T G A C G
 SEQ. ID. NO. 36 C C C A A C A C C A C C C G G C T C T G T G A C G
 SEQ. ID. NO. 32 A T C A G C A G T G T C G A G A C C C C T T A C A

SEQ. ID. NO. 40 T A T A T T C C A T G G C T T A C G C C C T G C A
 SEQ. ID. NO. 46 C G A T G C G G C C A G T T A A C G G G C G C C G
 SEQ. ID. NO. 36 C G A T G C G G C C A G T T A A C G G G C G C C G
 SEQ. ID. NO. 32 T A G A T T A C A C G C A T T T A C G G A T A T C

SEQ. ID. NO. 40 C A A T A T G C A C A A A G A T C T C T G C C C T
 SEQ. ID. NO. 46 C C T C T A C A A G G A C T T T G T G C T C A A C
 SEQ. ID. NO. 36 C C T C T A C A A G G A C T T T G T G C T C A A C
 SEQ. ID. NO. 32 C T A C A A T G T G T A C T T A G C A G T C T A C

SEQ. ID. NO. 40 G G A T A C A T T G G C C T T T G T C C A C G A A
 SEQ. ID. NO. 46 G T C A A G T T T G A T G C C C C C T T T C G C C
 SEQ. ID. NO. 36 G T C A A G T T T G A T G C C C C C T T T C G C C
 SEQ. ID. NO. 32 T C C A T T G C C C A C G C C T T G C A A G A T A

SEQ. ID. NO. 40 T G A G T A C C A T T G A T G G G A A A G A G C T
 SEQ. ID. NO. 46 C A G C T G A C A C C C A C A A T G A G G T C C G
 SEQ. ID. NO. 36 C A G C T G A C A C C C A C A A T G A G G T C C G
 SEQ. ID. NO. 32 T A T A T A C C T G C T T A C C T G G G A G A G G

SEQ. ID. NO. 40 A C T T G G T T A T A T T C G G G C T G T A A A T
 SEQ. ID. NO. 46 C T T T G A C C G C T T T G G T G A T G G T A T T
 SEQ. ID. NO. 36 C T T T G A C C G C T T T G G T G A T G G T A T T
 SEQ. ID. NO. 32 G C T C T T C A C C A A T G G C T C C T G T G C A

SEQ. ID. NO. 40 T T T A A T G G C A G T G C T G G C A C T C C T G
 SEQ. ID. NO. 46 G G C C G C T A C A A C A T C T T C A C C T A T C
 SEQ. ID. NO. 36 G G C C G C T A C A A C A T C T T C A C C T A T C
 SEQ. ID. NO. 32 G A C A T C A A G A A A G T T G A G G C G T G G C

SEQ. ID. NO. 40 T C A C T T T T A A T G A A A A C G G A G A T G C
 SEQ. ID. NO. 46 T G C G T G C A G G C A G T G G G C G C T A T C G
 SEQ. ID. NO. 36 T G C G T G C A G G C A G T G G G C G C T A T C G
 SEQ. ID. NO. 32 A G G T C C T G A A G C A C C T A C G G C A T C T

Figure 11g

SEQ. ID. NO. 40 T C C T G G A C G T T A T G A T A T C T T C C A G
 SEQ. ID. NO. 46 C T A C C A G A A G G T G G G C T A C T G G G C A
 SEQ. ID. NO. 36 C T A C C A G A A G G T G G G C T A C T G G G C A
 SEQ. ID. NO. 32 A A A C T T T A C A A A C A A T A T G G G G G A G

SEQ. ID. NO. 40 T A T C A A A T A A C C A A C A A A A G C A C A G
 SEQ. ID. NO. 46 G A A G G C T T G A C T C T G G A C A C C A G C C
 SEQ. ID. NO. 36 G A A G G C T T G A C T C T G G A C A C C A G C C
 SEQ. ID. NO. 32 C A G G T G A C C T T T G A T G A G T G T G G T G

SEQ. ID. NO. 40 A G T A C A A A G T C A T C G G C C A C T G G A C
 SEQ. ID. NO. 46 T C A T C C C A T G G G C C T C A C C C T C A G C
 SEQ. ID. NO. 36 T C A T C C C A T G G G C C T C A C C C T C A G C
 SEQ. ID. NO. 32 A C C T G G T G G G G A A C T A T T C C A T C A T

SEQ. ID. NO. 40 C A A T C A G C T T C A T C T A A A A G T G G A A
 SEQ. ID. NO. 46 C G G C C C C C T G C C C G C C T C T C G C T G C
 SEQ. ID. NO. 36 C G G C C C C C T G C C C G C C T C T C G C T G C
 SEQ. ID. NO. 32 C A A C T G G C A C C T C T C C C C A G A G G A T

SEQ. ID. NO. 40 G A C A T G C A G T G G G C T C A T A G A G A A C
 SEQ. ID. NO. 46 A G T G A G C C C T G C C T C C A G A A T G A G G
 SEQ. ID. NO. 36 A G T G A G C C C T G C C T C C A G A A T G A G G
 SEQ. ID. NO. 32 G G C T C C A T C G T G T T T A A G G A A G T C G

SEQ. ID. NO. 40 A T A C T C A C C C G G C G T C T G T C T G C A G
 SEQ. ID. NO. 46 T G A A G A G T G T G C A G C C G G G C G A A G T
 SEQ. ID. NO. 36 T G A A G A G T G T G C A G C C G G G C G A A G T
 SEQ. ID. NO. 32 G G T A T T A C A A C G T C T A T G C C A A G A A

SEQ. ID. NO. 40 C C T G C C G T G T A A G C C A G G G G A G A G G
 SEQ. ID. NO. 46 C T G C T G C T G G C T C T G C A T T C C G T G C
 SEQ. ID. NO. 36 C T G C T G C T G G C T C T G C A T T C C G T G C
 SEQ. ID. NO. 32 G G G A G A A A G A C T C T T C A T C A A C G A G

SEQ. ID. NO. 40 A A G A A A A C G G T G A A A G G G G T C C C T T
 SEQ. ID. NO. 46 C A G C C C T A T G A G T A C C G A T T G G A C G
 SEQ. ID. NO. 36 C A G C C C T A T G A G T A C C G A T T G G A C G
 SEQ. ID. NO. 32 G A G A A A A T C C T G T G G A G T G G G T T C T

Figure 11h

SEQ. ID. NO. 40 G C T G C T G G C A C T G T G A A C G C T G T G A
 SEQ. ID. NO. 46 A A T T C A C T T G C G C T G A T T G T G G C C T
 SEQ. ID. NO. 36 A A T T C A C T T G C G C T G A T T G T G G C C T
 SEQ. ID. NO. 32 C C A G G G A G G T G C C C T T C T C C A A C T G

SEQ. ID. NO. 40 A G G T T A C A A C T A C C A G G T G G A T G A G
 SEQ. ID. NO. 46 G G G C T A C T G G C C C A A T G C C A G C C T G
 SEQ. ID. NO. 36 G G G C T A C T G G C C C A A T G C C A G C C T G
 SEQ. ID. NO. 32 C A G C C G A G A C T G C C T G G C A G G G A C C

SEQ. ID. NO. 40 C T G T C C T G T G A A C T T T G C C C T C T G G
 SEQ. ID. NO. 46 A C T G G C T G C T T C G A A C T G C C C C A G G
 SEQ. ID. NO. 36 A C T G G C T G C T T C G A A C T G C C C C A G G
 SEQ. ID. NO. 32 A G G A A A G G G A T C A T T G A G G G G G A G C

SEQ. ID. NO. 40 A T C A G A G A C C C A A C A T G A A C C G C A C
 SEQ. ID. NO. 46 A G T A C A T C C G C T G G G G C G A T G C C T G
 SEQ. ID. NO. 36 A G T A C A T C C G C T G G G G C G A T G C C T G
 SEQ. ID. NO. 32 C C A C C T G C T G C T T T G A G T G T G T G G A

SEQ. ID. NO. 40 A G G C T G C C A G C T T A T C C C C A T C A T C
 SEQ. ID. NO. 46 G G C T G T G G G A C C T G T C A C C A T C G C C
 SEQ. ID. NO. 36 G G C T G T G G G A C C T G T C A C C A T C G C C
 SEQ. ID. NO. 32 G T G T C C T G A T G G G G A G T A T A G T G A T

SEQ. ID. NO. 40 A A A T T G G A G T G G C A T T C T C C C T G G G
 SEQ. ID. NO. 46 T G C C T C G G T G C C C T G G C C A C C C T C T
 SEQ. ID. NO. 36 T G C C T C G G T G C C C T G G C C A C C C T C T
 SEQ. ID. NO. 32 G A G A C A G A T G C C A G T G C C T G T A A C A

SEQ. ID. NO. 40 C T G T G G T G C C T G T G T T T G T T G C A A T
 SEQ. ID. NO. 46 T T G T G C T G G G T G T C T T T G T G C G G C A
 SEQ. ID. NO. 36 T T G T G C T G G G T G T C T T T G T G C G G C A
 SEQ. ID. NO. 32 A G T G C C C A G A T G A C T T C T G G T C C A A

SEQ. ID. NO. 40 A T T G G G A A T C A T C G C C A C C A C C T T T
 SEQ. ID. NO. 46 C A A T G C C A C A C C A G T G G T C A A G G C C
 SEQ. ID. NO. 36 C A A T G C C A C A C C A G T G G T C A A G G C C
 SEQ. ID. NO. 32 T G A G A A C C A C A C C T C C T G C T T C G A A

Figure 11i

SEQ. ID. NO. 40 G T G A T C G T G A C C T T T G T C C G C T A T A
 SEQ. ID. NO. 46 T C A G G T C G G G A G C T C T G C T A C A T C C
 SEQ. ID. NO. 36 T C A G G T C G G G A G C T C T G C T A C A T C C
 SEQ. ID. NO. 32 C T G C C C C A G G A G T A C A T C C G C T G G G

SEQ. ID. NO. 40 A T G A C A C A C C T A T C G T G A G G G C T T C
 SEQ. ID. NO. 46 T G C T G G G T G G T G T C T T C C T C T G C T A
 SEQ. ID. NO. 36 T G C T G G G T G G T G T C T T C C T C T G C T A
 SEQ. ID. NO. 32 G C G A T G C C T G G G C T G T G G G A C C T G T

SEQ. ID. NO. 40 A G G A C G C G A A C T T A G T T A C G T G C T C
 SEQ. ID. NO. 46 C T G C A T G A C C T T C A T C T T C A T T G C C
 SEQ. ID. NO. 36 C T G C A T G A C C T T C A T C T T C A T T G C C
 SEQ. ID. NO. 32 C A C C A T C G C C T G C C T C G G T G C C C T G

SEQ. ID. NO. 40 C T A A C G G G G A T T T T T C T C T G T T A T T
 SEQ. ID. NO. 46 A A G C C A T C C A C G G C A G T G T G T A C C T
 SEQ. ID. NO. 36 A A G C C A T C C A C G G C A G T G T G T A C C T
 SEQ. ID. NO. 32 G C C A C C C T G T T T G T G C T G G G T G T C T

SEQ. ID. NO. 40 C A A T C A C G T T T T T A A T G A T T G C A G C
 SEQ. ID. NO. 46 T A C G G C G T C T T G G T T T G G G C A C T G C
 SEQ. ID. NO. 36 T A C G G C G T C T T G G T T T G G G C A C T G C
 SEQ. ID. NO. 32 T T G T G C G G C A C A A T G C C A C A C C A G T

SEQ. ID. NO. 40 A C C A G A T A C A A T C A T A T G C T C C T T C
 SEQ. ID. NO. 46 C T T C T C T G T C T G C T A C T C A G C C C T G
 SEQ. ID. NO. 36 C T T C T C T G T C T G C T A C T C A G C C C T G
 SEQ. ID. NO. 32 G G T C A A G G C C T C A G G T C G G G A G C T C

SEQ. ID. NO. 40 C G A C G G G T C T T C C T A G G A C T T G G C A
 SEQ. ID. NO. 46 C T C A C C A A G A C C A A C C G C A T T G C A C
 SEQ. ID. NO. 36 C T C A C C A A G A C C A A C C G C A T T G C A C
 SEQ. ID. NO. 32 T G C T A C A T C C T G C T G G G T G G T G T C T

SEQ. ID. NO. 40 T G T G T T T C A G C T A T G C A G C C C T T C T
 SEQ. ID. NO. 46 G C A T C T T C G G T G G G G C C C G G G A G G G
 SEQ. ID. NO. 36 G C A T C T T C G G T G G G G C C C G G G A G G G
 SEQ. ID. NO. 32 T C C T C T G C T A C T G C A T G A C C T T C A T

Figure 11j

SEQ. ID. NO. 40 G A C C A A A A C A A A C C G T A T C C A C C G A
 SEQ. ID. NO. 46 T G C C C A G C G G C C A C G C T T C A T C A G T
 SEQ. ID. NO. 36 T G C C C A G C G G C C A C G C T T C A T C A G T
 SEQ. ID. NO. 32 C T T C A T T G C C A A G C C A T C C A C G G C A

SEQ. ID. NO. 40 A T A T T T G A G C A G G G G A A G A A A T C T G
 SEQ. ID. NO. 46 C C T G C C T C A C A G G T G G C C A T C T G C C
 SEQ. ID. NO. 36 C C T G C C T C A C A G G T G G C C A T C T G C C
 SEQ. ID. NO. 32 G T G T G T A C C T T A C G G C G T C T T G G T T

SEQ. ID. NO. 40 T C A C A G C G C C C A A G T T C A T T A G T C C
 SEQ. ID. NO. 46 T G G C A C T T A T C T C G G G C C A G C T G C T
 SEQ. ID. NO. 36 T G G C A C T T A T C T C G G G C C A G C T G C T
 SEQ. ID. NO. 32 T G G G C A C T G C C T T C T C T G T C T G C T A

SEQ. ID. NO. 40 A G C A T C T C A G C T G G T G A T C A C C T T C
 SEQ. ID. NO. 46 C A T C G T G G T C G C C T G G C T G G T G G T G
 SEQ. ID. NO. 36 C A T C G T G G T C G C C T G G C T G G T G G T G
 SEQ. ID. NO. 32 C T C A G C C C T G C T C A C C A A G A C C A A C

SEQ. ID. NO. 40 A G C C T C A T C T C C G T C C A G C T C C T T G
 SEQ. ID. NO. 46 G A G G C A C C G G G C A C A G G C A A G G A G A
 SEQ. ID. NO. 36 G A G G C A C C G G G C A C A G G C A A G G A G A
 SEQ. ID. NO. 32 C G C A T T G C A C G C A T C T T C G G T G G G G

SEQ. ID. NO. 40 G A G T G T T T G T C T G G T T T G T T G T G G A
 SEQ. ID. NO. 46 C A G C C C C C G A A C G G C G G G A G G T G G T
 SEQ. ID. NO. 36 C A G C C C C C G A A C G G C G G G A G G T G G T
 SEQ. ID. NO. 32 C C C G G G A G G G T G C C C A G C G G C C A C G

SEQ. ID. NO. 40 T C C C C C C C A C A T C A T C A T T G A C T A T
 SEQ. ID. NO. 46 G A C A C T G C G C T G C A A C C A C C G C G A T
 SEQ. ID. NO. 36 G A C A C T G C G C T G C A A C C A C C G C G A T
 SEQ. ID. NO. 32 C T T C A T C A G T C C T G C C T C A C A G G T G

SEQ. ID. NO. 40 G G A G A G C A G C G G A C A C T A G A T C C A G
 SEQ. ID. NO. 46 G C A A G T A T G T T G G G C T C G C T G G C C T
 SEQ. ID. NO. 36 G C A A G T A T G T T G G G C T C G C T G G C C T
 SEQ. ID. NO. 32 G C C A T C T G C C T G G C A C T T A T C T C G G

Figure 11k

SEQ. ID. NO. 40 A G A A G G C C A G G G G A G T G C T C A A G T G
 SEQ. ID. NO. 46 A C A A T G T G C T C C T C A T C G C G C T C T G
 SEQ. ID. NO. 36 A C A A T G T G C T C C T C A T C G C G C T C T G
 SEQ. ID. NO. 32 G C C A G C T G C T C A T C G T G G T C G C C T G

SEQ. ID. NO. 40 T G A C A T T T C T G A T C T C T C A C T C A T T
 SEQ. ID. NO. 46 C A C G C T T T A T G C C T T C A A G A C T C G C
 SEQ. ID. NO. 36 C A C G C T T T A T G C C T T C A A G A C T C G C
 SEQ. ID. NO. 32 G C T G G T G G T G G A G G C A C C G G G C A C A

SEQ. ID. NO. 40 T G T T C A C T T G G A T A C A G T A T C C T C T
 SEQ. ID. NO. 46 A A G T G C C C C G A A A A C T T C A A C G A G G
 SEQ. ID. NO. 36 A A G T G C C C C G A A A A C T T C A A C G A G G
 SEQ. ID. NO. 32 G G C A A G G A G A C A G C C C C C G A A C G G C

SEQ. ID. NO. 40 T G A T G G T C A C T T G T A C T G T T T A T G C
 SEQ. ID. NO. 46 C C A A G T T C A T T G G C T T C A C C A T G T A
 SEQ. ID. NO. 36 C C A A G T T C A T T G G C T T C A C C A T G T A
 SEQ. ID. NO. 32 G G G A G G T G G T G A C A C T G C G C T G C A A

SEQ. ID. NO. 40 C A T T A A A A C G A G A G G T G T C C C A G A G
 SEQ. ID. NO. 46 C A C C A C C T G C A T C A T C T G G C T G G C A
 SEQ. ID. NO. 36 C A C C A C C T G C A T C A T C T G G C T G G C A
 SEQ. ID. NO. 32 C C A C C G C G A T G C A A G T A T G T T G G G C

SEQ. ID. NO. 40 A C T T T C A A T G A A G C C A A A C C T A T T G
 SEQ. ID. NO. 46 T T C C T G C C C A T C T T C T A T G T C A C C T
 SEQ. ID. NO. 36 T T C C T G C C C A T C T T C T A T G T C A C C T
 SEQ. ID. NO. 32 T C G C T G G C C T A C A A T G T G C T C C T C A

SEQ. ID. NO. 40 G A T T T A C C A T G T A T A C C A C C T G C A T
 SEQ. ID. NO. 46 C C A G T G A C T A C C G G G T A C A G A C C A C
 SEQ. ID. NO. 36 C C A G T G A C T A C C G G G T A C A G A C C A C
 SEQ. ID. NO. 32 T C G C G C T C T G C A C G C T T T A T G C C T T

SEQ. ID. NO. 40 C A T T T G G T T A G C T T T C A T C C C C A T C
 SEQ. ID. NO. 46 C A C C A T G T G C G T G T C A G T C A G C C T C
 SEQ. ID. NO. 36 C A C C A T G T G C G T G T C A G T C A G C C T C
 SEQ. ID. NO. 32 C A A T A C T C G C A A G T G C C C C G A A A A C

Figure 11L

SEQ. ID. NO. 40 T T T T T T G G T A C A G C C C A G T C A G C A G
 SEQ. ID. NO. 46 A G C G G C T C C G T G G T G C T T G G C T G C C
 SEQ. ID. NO. 36 A G C G G C T C C G T G G T G C T T G G C T G C C
 SEQ. ID. NO. 32 T T C A A C G A G G C C A A G T T C A T T G G C T

SEQ. ID. NO. 40 A A A A G A T G T A C A T C C A G A C A A C A A C
 SEQ. ID. NO. 46 T C T T T G C G C C C A A G C T G C A C A T C A T
 SEQ. ID. NO. 36 T C T T T G C G C C C A A G C T G C A C A T C A T
 SEQ. ID. NO. 32 T C A C C A T G T A C A C C A C C T G C A T C A T

SEQ. ID. NO. 40 A C T T A C T G T C T C C A T G A G T T T A A G T
 SEQ. ID. NO. 46 C C T C T T C C A G C C G C A G A A G A A C A C C
 SEQ. ID. NO. 36 C C T C T T C C A G C C G C A G A A G A A C A C C
 SEQ. ID. NO. 32 C T G G C T G G C A T T G T T G C C C A T C T T C

SEQ. ID. NO. 40 G C T T C A G T A T C T C T G G G C A T G C T C T
 SEQ. ID. NO. 46 A T C G A G G A G G T G C G T T G C A G C A C C G
 SEQ. ID. NO. 36 A T C G A G G A G G T G C G T T G C A G C A C C G
 SEQ. ID. NO. 32 T A T G T C A C C T C C A G T G A C T A C C G G G

SEQ. ID. NO. 40 A T A T G C C C A A G G T T T A T A T T A T A A T
 SEQ. ID. NO. 46 C A G C T C A C G C T T T C A A G G T G G C T G C
 SEQ. ID. NO. 36 C A G C T C A C G C T T T C A A G G T G G C T G C
 SEQ. ID. NO. 32 T A C A G A C C A C C A C C A T G T G C G T G T C

SEQ. ID. NO. 40 T T T T C A T C C A G A A C A G A A T A C C A T C
 SEQ. ID. NO. 46 C C G G G C C A C G C T G C G C C G C A G C A A C
 SEQ. ID. NO. 36 C C G G G C C A C G C T G C G C C G C A G C A A C
 SEQ. ID. NO. 32 A G T C A G C C T C A G C G G C T C C G T G G T G

SEQ. ID. NO. 40 G A G G A G G T G C G T T G C A G C A C C G C A G
 SEQ. ID. NO. 46 G T C T C C C G C A A G C G G T C C A G C A G C C
 SEQ. ID. NO. 36 G T C T C C C G C A A G C G G T C C A G C A G C C
 SEQ. ID. NO. 32 C T T G G C T G C C T C T T T G C G C C C A A G C

SEQ. ID. NO. 40 C T C A C G C T T T C A A G G T G G C T G C C C G
 SEQ. ID. NO. 46 T T G G A G G C T C C A C G G G A T C C A C C C C
 SEQ. ID. NO. 36 T T G G A G G C T C C A C G G G A T C C A C C C C
 SEQ. ID. NO. 32 T G C A C A T C A T C C T C T T C C A G C C G C A

Figure 11m

SEQ. ID. NO. 40 G G C C A C G C T G C G C C G C A G C A A C G T C
 SEQ. ID. NO. 46 C T C C T C C T C C A T C A G C A G C A A G A G C
 SEQ. ID. NO. 36 C T C C T C C T C C A T C A G C A G C A A G A G C
 SEQ. ID. NO. 32 G A A G A A C G T G G T T A G C C A C C G G G C A

SEQ. ID. NO. 40 T C C C G C A A G C G G T C C A G C A G C C T T G
 SEQ. ID. NO. 46 A A C A G C G A A G A C C C A T T C C C A C A G C
 SEQ. ID. NO. 36 A A C A G C G A A G A C C C A T T C C C A C A G C
 SEQ. ID. NO. 32 C C C A C C A G C C G C T T T G G C A G T G C T G

SEQ. ID. NO. 40 G A G G C T C C A C G G G A T C C A C C C C C T C
 SEQ. ID. NO. 46 C C G A G A G G C A G A A G C A G C A G C A G C C
 SEQ. ID. NO. 36 C C G A G A G G C A G A A G C A G C A G C A G C C
 SEQ. ID. NO. 32 C T G C C A G G G C C A G C T C C A G C C T T G G

SEQ. ID. NO. 40 C T C C T C C A T C A G C A G C A A G A G C A A C
 SEQ. ID. NO. 46 G C T G G C C C T A A C C C A G C A A G A G C A G
 SEQ. ID. NO. 36 G C T G G C C C T A A C C C A G C A A G A G C A G
 SEQ. ID. NO. 32 C C A A G G G T C T G G C T C C C A G T T T G T C

SEQ. ID. NO. 40 A G C G A A G A C C C A T T C C C A C A G C C C G
 SEQ. ID. NO. 46 C A G C A G C A G C C C C T G A C C C T C C C A C
 SEQ. ID. NO. 36 C A G C A G C A G C C C C T G A C C C T C C C A C
 SEQ. ID. NO. 32 C C C A C T G T T T G C A A T G G C C G T G A G G

SEQ. ID. NO. 40 A G A G G C A G A A G C A G C A G C A G C C G C T
 SEQ. ID. NO. 46 A G C A G C A A C G A T C T C A G C A G C A G C C
 SEQ. ID. NO. 36 A G C A G C A A C G A T C T C A G C A G C A G C C
 SEQ. ID. NO. 32 T G G T G G A C T C G A C A A C G T C A T C G C T

SEQ. ID. NO. 40 G G C C C T A A C C C A G C A A G A G C A G C A G
 SEQ. ID. NO. 46 C A G A T G C A A G C A G A A G G T C A T C T T T
 SEQ. ID. NO. 36 C A G A T G C A A G C A G A A G G T C A T C T T T
 SEQ. ID. NO. 32 T A T G A C T C T G G A G T C C A T C A T G G C G

SEQ. ID. NO. 40 C A G C A G C C C C T G A C C C T C C C A C A G C
 SEQ. ID. NO. 46 G G C A G C G G C A C G G T C A C C T T C T C A C
 SEQ. ID. NO. 36 G G C A G C G G C A C G G T C A C C T T C T C A C
 SEQ. ID. NO. 32 T G C T G C C T G A G C G A G G A G G C C A A G G

Figure 11n

SEQ. ID. NO. 40 A G C A A C G A T C T C A G C A G C A G C C C A G
 SEQ. ID. NO. 46 T G A G C T T T G A T G A G C C T C A G A A G A A
 SEQ. ID. NO. 36 T G A G C T T T G A T G A G C C T C A G A A G A A
 SEQ. ID. NO. 32 A A G C C C G G C G G A T C A A C G A C G A G A T

SEQ. ID. NO. 40 A T G C A A G C A G A A G G T C A T C T T T G G C
 SEQ. ID. NO. 46 C G C C A T G G C C C A C G G G A A T T C T A C G
 SEQ. ID. NO. 36 C G C C A T G G C C C A C G G G A A T T C T A C G
 SEQ. ID. NO. 32 C G A G C G G C A G C T C C G C A G G G A C A A G

SEQ. ID. NO. 40 A G C G G C A C G G T C A C C T T C T C A C T G A
 SEQ. ID. NO. 46 C A C C A G A A C T C C C T G G A G G C C C A G A
 SEQ. ID. NO. 36 C A C C A G A A C T C C C T G G A G G C C C A G A
 SEQ. ID. NO. 32 C G G G A C G C C C G C C G G G A G C T C A A G C

SEQ. ID. NO. 40 G C T T T G A T G A G C C T C A G A A G A A C G C
 SEQ. ID. NO. 46 A A A G C A G C G A T A C G C T G A C C C G A C A
 SEQ. ID. NO. 36 A A A G C A G C G A T A C G C T G A C C C G A C A
 SEQ. ID. NO. 32 T G C T G C T G C T C G G G A C A G G A G A G A G

SEQ. ID. NO. 40 C A T G G C C C A C G G G A A T T C T A C G C A C
 SEQ. ID. NO. 46 C C A G C C A T T A C T C C C G C T G C A G T G C
 SEQ. ID. NO. 36 C C A G C C A T T A C T C C C G C T G C A G T G C
 SEQ. ID. NO. 32 T G G C A A G A G T A C G T T T A T C A A G C A G

SEQ. ID. NO. 40 C A G A A C T C C C T G G A G G C C C A G A A A A
 SEQ. ID. NO. 46 G G G G A A A C G G A C T T A G A T C T G A C C G
 SEQ. ID. NO. 36 G G G G A A A C G G A C T T A G A T C T G A C C G
 SEQ. ID. NO. 32 A T G A G A A T C A T C C A T G G G T C A G G A T

SEQ. ID. NO. 40 G C A G C G A T A C G C T G A C C C G A C A C C A
 SEQ. ID. NO. 46 T C C A G G A A A C A G G T C T G C A A G G A C C
 SEQ. ID. NO. 36 T C C A G G A A A C A G G T C T G C A A G G A C C
 SEQ. ID. NO. 32 A C T C T G A T G A A G A T A A A A G G G G C T T

SEQ. ID. NO. 40 G C C A T T A C T C C C G C T G C A G T G C G G G
 SEQ. ID. NO. 46 T G T G G G T G G A G A C C A G C G G C C A G A G
 SEQ. ID. NO. 36 T G T G G G T G G A G A C C A G C G G C C A G A G
 SEQ. ID. NO. 32 C A C C A A G C T G G T G T A T C A G A A C A T C

Figure 11o

SEQ. ID. NO. 40 G A A A C G G A C T T A G A T C T G A C C G T C C
 SEQ. ID. NO. 46 G T G G A G G A C C C T G A A G A G T T G T C C C
 SEQ. ID. NO. 36 G T G G A G G A C C C T G A A G A G T T G T C C C
 SEQ. ID. NO. 32 T T C A C G G C C A T G C A G G C C A T G A T C A

SEQ. ID. NO. 40 A G G A A A C A G G T C T G C A A G G A C C T G T
 SEQ. ID. NO. 46 C A G C A C T T G T A G T G T C C A G T T C A C A
 SEQ. ID. NO. 36 C A G C A C T T G T A G T G T C C A G T T C A C A
 SEQ. ID. NO. 32 G A G C C A T G G A C A C A C T C A A G A T C C C

SEQ. ID. NO. 40 G G G T G G A G A C C A G C G G C C A G A G G T G
 SEQ. ID. NO. 46 G A G C T T T G T C A T C A G T G G T G G A G G C
 SEQ. ID. NO. 36 G A G C T T T G T C A T C A G T G G T G G A G G C
 SEQ. ID. NO. 32 A T A C A A G T A T G A G C A C A A T A A G G C T

SEQ. ID. NO. 40 G A G G A C C C T G A A G A G T T G T C C C C A G
 SEQ. ID. NO. 46 A G C A C T G T T A C A G A A A A C G T A G T G A
 SEQ. ID. NO. 36 A G C A C T G T T A C A G A A A A C G T A G T G A
 SEQ. ID. NO. 32 C A T G C A C A A T T A G T T C G A G A A G T T G

SEQ. ID. NO. 40 C A C T T G T A G T G T C C A G T T C A C A G A G
 SEQ. ID. NO. 46 A T T C A G C G G C C G C C A T G A C T C T G G A
 SEQ. ID. NO. 36 A T T C A A T G A C T C T G G A G T C C A T C A T
 SEQ. ID. NO. 32 A T G T G G A G A A G G T G T C T G C T T T T G A

SEQ. ID. NO. 40 C T T T G T C A T C A G T G G T G G A G G C A G C
 SEQ. ID. NO. 46 G T C C A T C A T G G C G T G C T G C C T G A G C
 SEQ. ID. NO. 36 G G C G T G C T G C C T G A G C G A G G A G G C C
 SEQ. ID. NO. 32 G A A T C C A T A T G T A G A T G C A A T A A A G

SEQ. ID. NO. 40 A C T G T T A C A G A A A A C G T A G T G A A T T
 SEQ. ID. NO. 46 G A G G A G G C C A A G G A A G C C C G G C G G A
 SEQ. ID. NO. 36 A A G G A A G C C C G G C G G A T C A A C G A C G
 SEQ. ID. NO. 32 A G T T T A T G G A A T G A T C C T G G A A T C C

SEQ. ID. NO. 40 C A - - - - -
 SEQ. ID. NO. 46 T C A A C G A C G A G A T C G A G C G G C A G C T
 SEQ. ID. NO. 36 A G A T C G A G C G G C A G C T C C G C A G G G A
 SEQ. ID. NO. 32 A G G A A T G C T A T G A T A G A C G A C G A G A

Figure 11p

SEQ. ID. NO. 40 - - - - -
 SEQ. ID. NO. 46 C C G C A G G G A C A A G C G G G A C G C C C G C
 SEQ. ID. NO. 36 C A A G C G G G A C G C C C G C C G G G A G C T C
 SEQ. ID. NO. 32 A T A T C A A T T A T C T G A C T C T A C C A A A

SEQ. ID. NO. 40 - - - - - A T G A C T C T G G
 SEQ. ID. NO. 46 C G G G A G C T C A A G C T G C T G C T G C T C G
 SEQ. ID. NO. 36 A A G C T G C T G C T G C T C G G G A C A G G A G
 SEQ. ID. NO. 32 T A C T A T C T T A A T G A C T T G G A C C G C G

SEQ. ID. NO. 40 A G T C C A T C A T G G C G T G C T G C C T G A G
 SEQ. ID. NO. 46 G G A C A G G A G A G A G T G G C A A G A G T A C
 SEQ. ID. NO. 36 A G A G T G G C A A G A G T A C G T T T A T C A A
 SEQ. ID. NO. 32 T A G C T G A C C C T G C C T A C C T G C C T A C

SEQ. ID. NO. 40 C G A G G A G G C C A A G G A A G C C C G G C G G
 SEQ. ID. NO. 46 G T T T A T C A A G C A G A T G A G A A T C A T C
 SEQ. ID. NO. 36 G C A G A T G A G A A T C A T C C A T G G G T C A
 SEQ. ID. NO. 32 G C A A C A A G A T G T G C T T A G A G T T C G A

SEQ. ID. NO. 40 A T C A A C G A C G A G A T C G A G C G G C A G C
 SEQ. ID. NO. 46 C A T G G G T C A G G A T A C T C T G A T G A A G
 SEQ. ID. NO. 36 G G A T A C T C T G A T G A A G A T A A A A G G G
 SEQ. ID. NO. 32 G T C C C C A C C A C A G G G A T C A T C G A A T

SEQ. ID. NO. 40 T C C G C A G G G A C A A G C G G G A C G C C C G
 SEQ. ID. NO. 46 A T A A A A G G G G C T T C A C C A A G C T G G T
 SEQ. ID. NO. 36 G C T T C A C C A A G C T G G T G T A T C A G A A
 SEQ. ID. NO. 32 A C C C C T T T G A C T T A C A A A G T G T C A T

SEQ. ID. NO. 40 C C G G G A G C T C A A G C T G C T G C T G C T C
 SEQ. ID. NO. 46 G T A T C A G A A C A T C T T C A C G G C C A T G
 SEQ. ID. NO. 36 C A T C T T C A C G G C C A T G C A G G C C A T G
 SEQ. ID. NO. 32 T T T C A G A A T G G T C G A T G T A G G G G G C

SEQ. ID. NO. 40 G G G A C A G G A G A G A G T G G C A A G A G T A
 SEQ. ID. NO. 46 C A G G C C A T G A T C A G A G C C A T G G A C A
 SEQ. ID. NO. 36 A T C A G A G C C A T G G A C A C A C T C A A G A
 SEQ. ID. NO. 32 C A A A G G T C A G A G A G A A G A A A A T G G A

Figure 11q

SEQ. ID. NO. 40 C G T T T A T C A A G C A G A T G A G A A T C A T
 SEQ. ID. NO. 46 C A C T C A A G A T C C C A T A C A A G T A T G A
 SEQ. ID. NO. 36 T C C C A T A C A A G T A T G A G C A C A A T A A
 SEQ. ID. NO. 32 T A C A C T G C T T T G A A A A T G T C A C C T C

SEQ. ID. NO. 40 C C A T G G G T C A G G A T A C T C T G A T G A A
 SEQ. ID. NO. 46 G C A C A A T A A G G C T C A T G C A C A A T T A
 SEQ. ID. NO. 36 G G C T C A T G C A C A A T T A G T T C G A G A A
 SEQ. ID. NO. 32 T A T C A T G T T T C T A G T A G C G C T T A G T

SEQ. ID. NO. 40 G A T A A A A G G G G C T T C A C C A A G C T G G
 SEQ. ID. NO. 46 G T T C G A G A A G T T G A T G T G G A G A A G G
 SEQ. ID. NO. 36 G T T G A T G T G G A G A A G G T G T C T G C T T
 SEQ. ID. NO. 32 G A A T A T G A T C A A G T T C T C G T G G A G T

SEQ. ID. NO. 40 T G T A T C A G A A C A T C T T C A C G G C C A T
 SEQ. ID. NO. 46 T G T C T G C T T T T G A G A A T C C A T A T G T
 SEQ. ID. NO. 36 T T G A G A A T C C A T A T G T A G A T G C A A T
 SEQ. ID. NO. 32 C A G A C A A T G A G A A C C G A A T G G A G G A

SEQ. ID. NO. 40 G C A G G C C A T G A T C A G A G C C A T G G A C
 SEQ. ID. NO. 46 A G A T G C A A T A A A G A G T T T A T G G A A T
 SEQ. ID. NO. 36 A A A G A G T T T A T G G A A T G A T C C T G G A
 SEQ. ID. NO. 32 A A G C A A G G C T C T C T T T A G A A C A A T T

SEQ. ID. NO. 40 A C A C T C A A G A T C C C A T A C A A G T A T G
 SEQ. ID. NO. 46 G A T C C T G G A A T C C A G G A A T G C T A T G
 SEQ. ID. NO. 36 A T C C A G G A A T G C T A T G A T A G A C G A C
 SEQ. ID. NO. 32 A T C A C A T A C C C C T G G T T C C A G A A C T

SEQ. ID. NO. 40 A G C A C A A T A A G G C T C A T G C A C A A T T
 SEQ. ID. NO. 46 A T A G A C G A C G A G A A T A T C A A T T A T C
 SEQ. ID. NO. 36 G A G A A T A T C A A T T A T C T G A C T C T A C
 SEQ. ID. NO. 32 C C T C G G T T A T T C T G T T C T T A A A C A A

SEQ. ID. NO. 40 A G T T C G A G A A G T T G A T G T G G A G A A G
 SEQ. ID. NO. 46 T G A C T C T A C C A A A T A C T A T C T T A A T
 SEQ. ID. NO. 36 C A A A T A C T A T C T T A A T G A C T T G G A C
 SEQ. ID. NO. 32 G A A A G A T C T T C T A G A G G A G A A A A T C

Figure 11r

SEQ. ID. NO. 40 G T G T C T G C T T T T G A G A A T C C A T A T G
 SEQ. ID. NO. 46 G A C T T G G A C C G C G T A G C T G A C C C T G
 SEQ. ID. NO. 36 C G C G T A G C T G A C C C T G C C T A C C T G C
 SEQ. ID. NO. 32 A T G T A T T C C C A T C T A G T C G A C T A C T

SEQ. ID. NO. 40 T A G A T G C A A T A A A G A G T T T A T G G A A
 SEQ. ID. NO. 46 C C T A C C T G C C T A C G C A A C A A G A T G T
 SEQ. ID. NO. 36 C T A C G C A A C A A G A T G T G C T T A G A G T
 SEQ. ID. NO. 32 T C C C A G A A T A T G A T G G A C C C C A G A G

SEQ. ID. NO. 40 T G A T C C T G G A A T C C A G G A A T G C T A T
 SEQ. ID. NO. 46 G C T T A G A G T T C G A G T C C C C A C C A C A
 SEQ. ID. NO. 36 T C G A G T C C C C A C C A C A G G G A T C A T C
 SEQ. ID. NO. 32 A G A T G C C C A G G C A G C C C G A G A A T T C

SEQ. ID. NO. 40 G A T A G A C G A C G A G A A T A T C A A T T A T
 SEQ. ID. NO. 46 G G G A T C A T C G A A T A C C C C T T T G A C T
 SEQ. ID. NO. 36 G A A T A C C C C T T T G A C T T A C A A A G T G
 SEQ. ID. NO. 32 A T T C T G A A G A T G T T C G T G G A C C T G A

SEQ. ID. NO. 40 C T G A C T C T A C C A A A T A C T A T C T T A A
 SEQ. ID. NO. 46 T A C A A A G T G T C A T T T T C A G A A T G G T
 SEQ. ID. NO. 36 T C A T T T T C A G A A T G G T C G A T G T A G G
 SEQ. ID. NO. 32 A C C C A G A C A G T G A C A A A A T T A T C T A

SEQ. ID. NO. 40 T G A C T T G G A C C G C G T A G C T G A C C C T
 SEQ. ID. NO. 46 C G A T G T A G G G G G C C A A A G G T C A G A G
 SEQ. ID. NO. 36 G G G C C A A A G G T C A G A G A G A A G A A A A
 SEQ. ID. NO. 32 C T C C C A C T T C A C G T G C G C C A C A G A C

SEQ. ID. NO. 40 G C C T A C C T G C C T A C G C A A C A A G A T G
 SEQ. ID. NO. 46 A G A A G A A A A T G G A T A C A C T G C T T T G
 SEQ. ID. NO. 36 T G G A T A C A C T G C T T T G A A A A T G T C A
 SEQ. ID. NO. 32 A C C G A G A A T A T C C G C T T T G T C T T T G

SEQ. ID. NO. 40 T G C T T A G A G T T C G A G T C C C C A C C A C
 SEQ. ID. NO. 46 A A A A T G T C A C C T C T A T C A T G T T T C T
 SEQ. ID. NO. 36 C C T C T A T C A T G T T T C T A G T A G C G C T
 SEQ. ID. NO. 32 C T G C C G T C A A G G A C A C C A T C C T C C A

Figure 11s

SEQ. ID. NO. 40 A G G G A T C A T C G A A T A C C C C T T T G A C
 SEQ. ID. NO. 46 A G T A G C G C T T A G T G A A T A T G A T C A A
 SEQ. ID. NO. 36 T A G T G A A T A T G A T C A A G T T C T C G T G
 SEQ. ID. NO. 32 G T T G A A C C T G A A G G A C T G C G G T C T G

SEQ. ID. NO. 40 T T A C A A A G T G T C A T T T T C A G A A T G G
 SEQ. ID. NO. 46 G T T C T C G T G G A G T C A G A C A A T G A G A
 SEQ. ID. NO. 36 G A G T C A G A C A A T G A G A A C C G A A T G G
 SEQ. ID. NO. 32 T T C T A A

SEQ. ID. NO. 40 T C G A T G T A G G G G G C C A A A G G T C A G A
 SEQ. ID. NO. 46 A C C G A A T G G A G G A A A G C A A G G C T C T
 SEQ. ID. NO. 36 A G G A A A G C A A G G C T C T C T T T A G A A C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A G A A G A A A A T G G A T A C A C T G C T T T
 SEQ. ID. NO. 46 C T T T A G A A C A A T T A T C A C A T A C C C C
 SEQ. ID. NO. 36 A A T T A T C A C A T A C C C C T G G T T C C A G
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A A A A T G T C A C C T C T A T C A T G T T T C
 SEQ. ID. NO. 46 T G G T T C C A G A A C T C C T C G G T T A T T C
 SEQ. ID. NO. 36 A A C T C C T C G G T T A T T C T G T T C T T A A
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 T A G T A G C G C T T A G T G A A T A T G A T C A
 SEQ. ID. NO. 46 T G T T C T T A A A C A A G A A A G A T C T T C T
 SEQ. ID. NO. 36 A C A A G A A A G A T C T T C T A G A G G A G A A
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 A G T T C T C G T G G A G T C A G A C A A T G A G
 SEQ. ID. NO. 46 A G A G G A G A A A A T C A T G T A T T C C C A T
 SEQ. ID. NO. 36 A A T C A T G T A T T C C C A T C T A G T C G A C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 A A C C G A A T G G A G G A A A G C A A G G C T C
 SEQ. ID. NO. 46 C T A G T C G A C T A C T T C C C A G A A T A T G
 SEQ. ID. NO. 36 T A C T T C C C A G A A T A T G A T G G A C C C C
 SEQ. ID. NO. 32

Figure 11t

SEQ. ID. NO. 40 T C T T T A G A A C A A T T A T C A C A T A C C C
 SEQ. ID. NO. 46 A T G G A C C C C A G A G A G A T G C C C A G G C
 SEQ. ID. NO. 36 A G A G A G A T G C C C A G G C A G C C C G A G A
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 C T G G T T C C A G A A C T C C T C G G T T A T T
 SEQ. ID. NO. 46 A G C C C G A G A A T T C A T T C T G A A G A T G
 SEQ. ID. NO. 36 A T T C A T T C T G A A G A T G T T C G T G G A C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 C T G T T C T T A A A C A A G A A A G A T C T T C
 SEQ. ID. NO. 46 T T C G T G G A C C T G A A C C C A G A C A G T G
 SEQ. ID. NO. 36 C T G A A C C C A G A C A G T G A C A A A A T T A
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 T A G A G G A G A A A A T C A T G T A T T C C C A
 SEQ. ID. NO. 46 A C A A A A T T A T C T A C T C C C A C T T C A C
 SEQ. ID. NO. 36 T C T A C T C C C A C T T C A C G T G C G C C A C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 T C T A G T C G A C T A C T T C C C A G A A T A T
 SEQ. ID. NO. 46 G T G C G C C A C A G A C A C C G A G A A T A T C
 SEQ. ID. NO. 36 A G A C A C C G A G A A T A T C C G C T T T G T C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A T G G A C C C C A G A G A G A T G C C C A G G
 SEQ. ID. NO. 46 C G C T T T G T C T T T G C T G C C G T C A A G G
 SEQ. ID. NO. 36 T T T G C T G C C G T C A A G G A C A C C A T C C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 C A G C C C G A G A A T T C A T T C T G A A G A T
 SEQ. ID. NO. 46 A C A C C A T C C T C C A G T T G A A C C T G A A
 SEQ. ID. NO. 36 T C C A G T T G A A C C T G A A G G A C T G C G G
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 G T T C G T G G A C C T G A A C C C A G A C A G T
 SEQ. ID. NO. 46 G G A C T G C G G T C T G T T C T A A T T G T G C
 SEQ. ID. NO. 36 T C T G T T C T A A
 SEQ. ID. NO. 32

Figure 11u

SEQ. ID. NO. 40 G A C A A A A T T A T C T A C T C C C A C T T C A
SEQ. ID. NO. 46 C T C C T A G A C A C C C G C C C T G C C C T T C
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C G T G C G C C A C A G A C A C C G A G A A T A T
SEQ. ID. NO. 46 C C T G G T
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C C G C T T T G T C T T T G C T G C C G T C A A G
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A C A C C A T C C T C C A G T T G A A C C T G A
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 A G G A C T G C G G T C T G T T C T A A
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

Figure 11v

ClustalW Formatted Alignments

SEQ. ID. NO. 41 M V C E G K R S A S C P C F F L L T A K F Y W I L
 SEQ. ID. NO. 47 M G S L L A L P A L L L L W G A V A E G P A K K V
 SEQ. ID. NO. 37 M G S L L A L P A L L L L W G A V A E G P A K K V
 SEQ. ID. NO. 33 M A F Y S C C W V L L A L T W H T S A Y G P D Q R

SEQ. ID. NO. 41 T M M Q R T H S Q E Y A H S I R V D G D I I L G G
 SEQ. ID. NO. 47 L T L E G D L V L G G L F P V H Q K G G P A E D C
 SEQ. ID. NO. 37 L T L E G D L V L G G L F P V H Q K G G P A E D C
 SEQ. ID. NO. 33 A Q K K G D I I L G G L F P I H F G V A A K D Q D

SEQ. ID. NO. 41 L F P V H A K G E R G V P C G E L K K E K G I H R
 SEQ. ID. NO. 47 G P V N E H R G I Q R L E A M L F A L D R I N R D
 SEQ. ID. NO. 37 G P V N E H R G I Q R L E A M L F A L D R I N R D
 SEQ. ID. NO. 33 L K S R P E S V E C I R Y N F R G F R W L Q A M I

SEQ. ID. NO. 41 L E A M L Y A I D Q I N K D P D L L S N I T L G V
 SEQ. ID. NO. 47 P H L L P G V R L G A H I L D S C S K D T H A L E
 SEQ. ID. NO. 37 P H L L P G V R L G A H I L D S C S K D T H A L E
 SEQ. ID. NO. 33 F A I E E I N S S P A L L P N L T L G Y R I F D T

SEQ. ID. NO. 41 R I L D T C S R D T Y A L E Q S L T F V Q A L I E
 SEQ. ID. NO. 47 Q A L D F V R A S L S R G A D G S R H I C P D G S
 SEQ. ID. NO. 37 Q A L D F V R A S L S R G A D G S R H I C P D G S
 SEQ. ID. NO. 33 C N T V S K A L E A T L S F V A Q N K I D S L N L

SEQ. ID. NO. 41 K D A S D V K C A N G D P P I F T K P D K I S G V
 SEQ. ID. NO. 47 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
 SEQ. ID. NO. 37 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
 SEQ. ID. NO. 33 D E F C N C S E H I P S T I A V V G A T G S G V S

SEQ. ID. NO. 41 I G A A A S S V S I M V A N I L R L F K I P Q I S
 SEQ. ID. NO. 47 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
 SEQ. ID. NO. 37 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
 SEQ. ID. NO. 33 T A V A N L L G L F Y I P Q V S Y A S S S R L L S

SEQ. ID. NO. 41 Y A S T A P E L S D N T R Y D F F S R V V P P D S
 SEQ. ID. NO. 47 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
 SEQ. ID. NO. 37 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
 SEQ. ID. NO. 33 N K N Q F K S F L R T I P N D E H Q A T A M A D I

Figure 12a

SEQ. ID. NO. 41 Y Q A Q A M V D I V T A L G W N Y V S T L A S E G
 SEQ. ID. NO. 47 F F N W T Y V S T V A S E G D Y G E T G I E A F E
 SEQ. ID. NO. 37 F F N W T Y V S T V A S E G D Y G E T G I E A F E
 SEQ. ID. NO. 33 I E Y F R W N W V G T I A A D D D Y G R P G I E K

SEQ. ID. NO. 41 N Y G E S G V E A F T Q I S R E I G G V C I A Q S
 SEQ. ID. NO. 47 L E A R A R N I C V A T S E K V G R A M S R A A F
 SEQ. ID. NO. 37 L E A R A R N I C V A T S E K V G R A M S R A A F
 SEQ. ID. NO. 33 F R E E A E E R D I C I D F S E L I S Q Y S D E E

SEQ. ID. NO. 41 Q K I P R E P R P G E F E K I I K R L L E T P N A
 SEQ. ID. NO. 47 E G V V R A L L Q K P S A R V A V L F T R S E D A
 SEQ. ID. NO. 37 E G V V R A L L Q K P S A R V A V L F T R S E D A
 SEQ. ID. NO. 33 E I Q H V V E V I Q N S T A K V I V V F S S G P D

SEQ. ID. NO. 41 R A V I M F A N E D D I R R I L E A A K K L N Q S
 SEQ. ID. NO. 47 R E L L A A S Q R L N A S F T W V A S D G W G A L
 SEQ. ID. NO. 37 R E L L A A S Q R L N A S F T W V A S D G W G A L
 SEQ. ID. NO. 33 L E P L I K E I V R R N I T G K I W L A S E A W A

SEQ. ID. NO. 41 G H F L W I G S D S W G S K I A P V Y Q Q E E I A
 SEQ. ID. NO. 47 E S V V A G S E G A A E G A I T I E L A S Y P I S
 SEQ. ID. NO. 37 E S V V A G S E G A A E G A I T I E L A S Y P I S
 SEQ. ID. NO. 33 S S S L I A M P Q Y F H V V G G T I G F A L K A G

SEQ. ID. NO. 41 E G A V T I L P K R A S I D G F D R Y F R S R T L
 SEQ. ID. NO. 47 D F A S Y F Q S L D P W N N S R N P W F R E F W E
 SEQ. ID. NO. 37 D F A S Y F Q S L D P W N N S R N P W F R E F W E
 SEQ. ID. NO. 33 Q I P G F R E F L K K V H P R K S V H N G F A K E

SEQ. ID. NO. 41 A N N R R N V W F A E F W E E N F G C K L G S H G
 SEQ. ID. NO. 47 Q R F R C S F R Q R D C A A H S L R A V P F E Q E
 SEQ. ID. NO. 37 Q R F R C S F R Q R D C A A H S L R A V P F E Q E
 SEQ. ID. NO. 33 F W E E T F N C H L Q E G A K G P L P V D T F L R

SEQ. ID. NO. 41 K R N S H I K K C T G L E R I A R D S S Y E Q E G
 SEQ. ID. NO. 47 S K I M F V V N A V Y A M A H A L H N M H R A L C
 SEQ. ID. NO. 37 S K I M F V V N A V Y A M A H A L H N M H R A L C
 SEQ. ID. NO. 33 G H E E S G D R F S N S S T A F R P L C T G D E N

Figure 12b

SEQ. ID. NO. 41 K V Q F V I D A V Y S M A Y A L H N M H K D L C P
 SEQ. ID. NO. 47 P N T T R L C D A M R P V N G R R L Y K D F V L N
 SEQ. ID. NO. 37 P N T T R L C D A M R P V N G R R L Y K D F V L N
 SEQ. ID. NO. 33 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y

SEQ. ID. NO. 41 G Y I G L C P R M S T I D G K E L L G Y I R A V N
 SEQ. ID. NO. 47 V K F D A P F R P A D T H N E V R F D R F G D G I
 SEQ. ID. NO. 37 V K F D A P F R P A D T H N E V R F D R F G D G I
 SEQ. ID. NO. 33 S I A H A L Q D I Y T C L P G R G L F T N G S C A

SEQ. ID. NO. 41 F N G S A G T P V T F N E N G D A P G R Y D I F Q
 SEQ. ID. NO. 47 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
 SEQ. ID. NO. 37 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
 SEQ. ID. NO. 33 D I K K V E A W Q V L K H L R H L N F T N N M G E

SEQ. ID. NO. 41 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E
 SEQ. ID. NO. 47 E G L T L D T S L I P W A S P S A G P L P A S R C
 SEQ. ID. NO. 37 E G L T L D T S L I P W A S P S A G P L P A S R C
 SEQ. ID. NO. 33 Q V T F D E C G D L V G N Y S I I N W H L S P E D

SEQ. ID. NO. 41 D M Q W A H R E H T H P A S V C S L P C K P G E R
 SEQ. ID. NO. 47 S E P C L Q N E V K S V Q P G E V C C W L C I P C
 SEQ. ID. NO. 37 S E P C L Q N E V K S V Q P G E V C C W L C I P C
 SEQ. ID. NO. 33 G S I V F K E V G Y Y N V Y A K K G E R L F I N E

SEQ. ID. NO. 41 K K T V K G V P C C W H C E R C E G Y N Y Q V D E
 SEQ. ID. NO. 47 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
 SEQ. ID. NO. 37 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
 SEQ. ID. NO. 33 E K I L W S G F S R E V P F S N C S R D C L A G T

SEQ. ID. NO. 41 L S C E L C P L D Q R P N M N R T G C Q L I P I I
 SEQ. ID. NO. 47 T G C F E L P Q E Y I R W G D A W A V G P V T I A
 SEQ. ID. NO. 37 T G C F E L P Q E Y I R W G D A W A V G P V T I A
 SEQ. ID. NO. 33 R K G I I E G E P T C C F E C V E C P D G E Y S D

SEQ. ID. NO. 41 K L E W H S P W A V V P V F V A I L G I I A T T F
 SEQ. ID. NO. 47 C L G A L A T L F V L G V F V R H N A T P V V K A
 SEQ. ID. NO. 37 C L G A L A T L F V L G V F V R H N A T P V V K A
 SEQ. ID. NO. 33 E T D A S A C N K C P D D F W S N E N H T S C F E

Figure 12c

SEQ. ID. NO. 41 V I V T F V R Y N D T P I V R A S G R E L S Y V L
 SEQ. ID. NO. 47 S G R E L C Y I L L G G V F L C Y C M T F I F I A
 SEQ. ID. NO. 37 S G R E L C Y I L L G G V F L C Y C M T F I F I A
 SEQ. ID. NO. 33 L P Q E Y I R W G D A W A V G P V T I A C L G A L

SEQ. ID. NO. 41 L T G I F L C Y S I T F L M I A A P D T I I C S F
 SEQ. ID. NO. 47 K P S T A V C T L R R L G L G T A F S V C Y S A L
 SEQ. ID. NO. 37 K P S T A V C T L R R L G L G T A F S V C Y S A L
 SEQ. ID. NO. 33 A T L F V L G V F V R H N A T P V V K A S G R E L

SEQ. ID. NO. 41 R R V F L G L G M C F S Y A A L L T K T N R I H R
 SEQ. ID. NO. 47 L T K T N R I A R I F G G A R E G A Q R P R F I S
 SEQ. ID. NO. 37 L T K T N R I A R I F G G A R E G A Q R P R F I S
 SEQ. ID. NO. 33 C Y I L L G G V F L C Y C M T F I F I A K P S T A

SEQ. ID. NO. 41 I F E Q G K K S V T A P K F I S P A S Q L V I T F
 SEQ. ID. NO. 47 P A S Q V A I C L A L I S G Q L L I V V A W L V V
 SEQ. ID. NO. 37 P A S Q V A I C L A L I S G Q L L I V V A W L V V
 SEQ. ID. NO. 33 V C T L R R L G L G T A F S V C Y S A L L T K T N

SEQ. ID. NO. 41 S L I S V Q L L G V F V W F V V D P P H I I I D Y
 SEQ. ID. NO. 47 E A P G T G K E T A P E R R E V V T L R C N H R D
 SEQ. ID. NO. 37 E A P G T G K E T A P E R R E V V T L R C N H R D
 SEQ. ID. NO. 33 R I A R I F G G A R E G A Q R P R F I S P A S Q V

SEQ. ID. NO. 41 G E Q R T L D P E K A R G V L K C D I S D L S L I
 SEQ. ID. NO. 47 A S M L G S L A Y N V L L I A L C T L Y A F K T R
 SEQ. ID. NO. 37 A S M L G S L A Y N V L L I A L C T L Y A F K T R
 SEQ. ID. NO. 33 A I C L A L I S G Q L L I V V A W L V V E A P G T

SEQ. ID. NO. 41 C S L G Y S I L L M V T C T V Y A I K T R G V P E
 SEQ. ID. NO. 47 K C P E N F N E A K F I G F T M Y T T C I I W L A
 SEQ. ID. NO. 37 K C P E N F N E A K F I G F T M Y T T C I I W L A
 SEQ. ID. NO. 33 G K E T A P E R R E V V T L R C N H R D A S M L G

SEQ. ID. NO. 41 T F N E A K P I G F T M Y T T C I I W L A F I P I
 SEQ. ID. NO. 47 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
 SEQ. ID. NO. 37 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
 SEQ. ID. NO. 33 S L A Y N V L L I A L C T L Y A F N T R K C P E N

Figure 12d

SEQ. ID. NO. 41 F F G T A Q S A E K M Y I Q T T T L T V S M S L S
 SEQ. ID. NO. 47 S G S V V L G C L F A P K L H I I L F Q P Q K N T
 SEQ. ID. NO. 37 S G S V V L G C L F A P K L H I I L F Q P Q K N T
 SEQ. ID. NO. 33 F N E A K F I G F T M Y T T C I I W L A L L P I F

SEQ. ID. NO. 41 A S V S L G M L Y M P K V Y I I I F H P E Q N T I
 SEQ. ID. NO. 47 I E E V R C S T A A H A F K V A A R A T L R R S N
 SEQ. ID. NO. 37 I E E V R C S T A A H A F K V A A R A T L R R S N
 SEQ. ID. NO. 33 Y V T S S D Y R V Q T T T M C V S V S L S G S V V

SEQ. ID. NO. 41 E E V R C S T A A H A F K V A A R A T L R R S N V
 SEQ. ID. NO. 47 V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 37 V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 33 L G C L F A P K L H I I L F Q P Q K N V V S H R A

SEQ. ID. NO. 41 S R K R S S S L G G S T G S T P S S S I S S K S N
 SEQ. ID. NO. 47 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
 SEQ. ID. NO. 37 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
 SEQ. ID. NO. 33 P T S R F G S A A A R A S S S L G Q G S G S Q F V

SEQ. ID. NO. 41 S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q
 SEQ. ID. NO. 47 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
 SEQ. ID. NO. 37 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
 SEQ. ID. NO. 33 P T V C N G R E V V D S T T S S L M T L E S I M A

SEQ. ID. NO. 41 Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F G
 SEQ. ID. NO. 47 G S G T V T F S L S F D E P Q K N A M A H G N S T
 SEQ. ID. NO. 37 G S G T V T F S L S F D E P Q K N A M A H G N S T
 SEQ. ID. NO. 33 C C L S E E A K E A R R I N D E I E R Q L R R D K

SEQ. ID. NO. 41 S G T V T F S L S F D E P Q K N A M A H G N S T H
 SEQ. ID. NO. 47 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
 SEQ. ID. NO. 37 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
 SEQ. ID. NO. 33 R D A R R E L K L L L L G T G E S G K S T F I K Q

SEQ. ID. NO. 41 Q N S L E A Q K S S D T L T R H Q P L L P L Q C G
 SEQ. ID. NO. 47 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
 SEQ. ID. NO. 37 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
 SEQ. ID. NO. 33 M R I I H G S G Y S D E D K R G F T K L V Y Q N I

Figure 12e

SEQ. ID. NO. 41 E T D L D L T V Q E T G L Q G P V G G D Q R P E V
 SEQ. ID. NO. 47 V E D P E E L S P A L V V S S S Q S F V I S G G G
 SEQ. ID. NO. 37 V E D P E E L S P A L V V S S S Q S F V I S G G G
 SEQ. ID. NO. 33 F T A M Q A M I R A M D T L K I P Y K Y E H N K A

SEQ. ID. NO. 41 E D P E E L S P A L V V S S S Q S F V I S G G G S
 SEQ. ID. NO. 47 S T V T E N V V N S A A A M T L E S I M A C C L S
 SEQ. ID. NO. 37 S T V T E N V V N S M T L E S I M A C C L S E E A
 SEQ. ID. NO. 33 H A Q L V R E V D V E K V S A F E N P Y V D A I K

SEQ. ID. NO. 41 T V T E N V V N S M T L E S I M A C C L S E E A K
 SEQ. ID. NO. 47 E E A K E A R R I N D E I E R Q L R R D K R D A R
 SEQ. ID. NO. 37 K E A R R I N D E I E R Q L R R D K R D A R R E L
 SEQ. ID. NO. 33 S L W N D P G I Q E C Y D R R R E Y Q L S D S T K

SEQ. ID. NO. 41 E A R R I N D E I E R Q L R R D K R D A R R E L K
 SEQ. ID. NO. 47 R E L K L L L L G T G E S G K S T F I K Q M R I I
 SEQ. ID. NO. 37 K L L L L G T G E S G K S T F I K Q M R I I H G S
 SEQ. ID. NO. 33 Y Y L N D L D R V A D P A Y L P T Q Q D V L R V R

SEQ. ID. NO. 41 L L L L G T G E S G K S T F I K Q M R I I H G S G
 SEQ. ID. NO. 47 H G S G Y S D E D K R G F T K L V Y Q N I F T A M
 SEQ. ID. NO. 37 G Y S D E D K R G F T K L V Y Q N I F T A M Q A M
 SEQ. ID. NO. 33 V P T T G I I E Y P F D L Q S V I F R M V D V G G

SEQ. ID. NO. 41 Y S D E D K R G F T K L V Y Q N I F T A M Q A M I
 SEQ. ID. NO. 47 Q A M I R A M D T L K I P Y K Y E H N K A H A Q L
 SEQ. ID. NO. 37 I R A M D T L K I P Y K Y E H N K A H A Q L V R E
 SEQ. ID. NO. 33 Q R S E R R K W I H C F E N V T S I M F L V A L S

SEQ. ID. NO. 41 R A M D T L K I P Y K Y E H N K A H A Q L V R E V
 SEQ. ID. NO. 47 V R E V D V E K V S A F E N P Y V D A I K S L W N
 SEQ. ID. NO. 37 V D V E K V S A F E N P Y V D A I K S L W N D P G
 SEQ. ID. NO. 33 E Y D Q V L V E S D N E N R M E E S K A L F R T I

SEQ. ID. NO. 41 D V E K V S A F E N P Y V D A I K S L W N D P G I
 SEQ. ID. NO. 47 D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N
 SEQ. ID. NO. 37 I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D
 SEQ. ID. NO. 33 I T Y P W F Q N S S V I L F L N K K D L L E E K I

Figure 12f

SEQ. ID. NO. 41 Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R
 SEQ. ID. NO. 47 D L D R V A D P A Y L P T Q Q D V L R V R V P T T
 SEQ. ID. NO. 37 R V A D P A Y L P T Q Q D V L R V R V P T T G I I
 SEQ. ID. NO. 33 M Y S H L V D Y F P E Y D G P Q R D A Q A A R E F

SEQ. ID. NO. 41 V A D P A Y L P T Q Q D V L R V R V P T T G I I E
 SEQ. ID. NO. 47 G I I E Y P F D L Q S V I F R M V D V G G Q R S E
 SEQ. ID. NO. 37 E Y P F D L Q S V I F R M V D V G G Q R S E R R K
 SEQ. ID. NO. 33 I L K M F V D L N P D S D K I I Y S H F T C A T D

SEQ. ID. NO. 41 Y P F D L Q S V I F R M V D V G G Q R S E R R K W
 SEQ. ID. NO. 47 R R K W I H C F E N V T S I M F L V A L S E Y D Q
 SEQ. ID. NO. 37 W I H C F E N V T S I M F L V A L S E Y D Q V L V
 SEQ. ID. NO. 33 T E N I R F V F A A V K D T I L Q L N L K D C G L

SEQ. ID. NO. 41 I H C F E N V T S I M F L V A L S E Y D Q V L V E
 SEQ. ID. NO. 47 V L V E S D N E N R M E E S K A L F R T I I T Y P
 SEQ. ID. NO. 37 E S D N E N R M E E S K A L F R T I I T Y P W F Q
 SEQ. ID. NO. 33 F

SEQ. ID. NO. 41 S D N E N R M E E S K A L F R T I I T Y P W F Q N
 SEQ. ID. NO. 47 W F Q N S S V I L F L N K K D L L E E K I M Y S H
 SEQ. ID. NO. 37 N S S V I L F L N K K D L L E E K I M Y S H L V D
 SEQ. ID. NO. 33

SEQ. ID. NO. 41 S S V I L F L N K K D L L E E K I M Y S H L V D Y
 SEQ. ID. NO. 47 L V D Y F P E Y D G P Q R D A Q A A R E F I L K M
 SEQ. ID. NO. 37 Y F P E Y D G P Q R D A Q A A R E F I L K M F V D
 SEQ. ID. NO. 33

SEQ. ID. NO. 41 F P E Y D G P Q R D A Q A A R E F I L K M F V D L
 SEQ. ID. NO. 47 F V D L N P D S D K I I Y S H F T C A T D T E N I
 SEQ. ID. NO. 37 L N P D S D K I I Y S H F T C A T D T E N I R F V
 SEQ. ID. NO. 33

SEQ. ID. NO. 41 N P D S D K I I Y S H F T C A T D T E N I R F V F
 SEQ. ID. NO. 47 R F V F A A V K D T I L Q L N L K D C G L F
 SEQ. ID. NO. 37 F A A V K D T I L Q L N L K D C G L F
 SEQ. ID. NO. 33

Figure 12g

SEQ. ID. NO. 41 A A V K D T I L Q L N L K D C G L F
SEQ. ID. NO. 47
SEQ. ID. NO. 37
SEQ. ID. NO. 33

Figure 12h

ClustalW Formatted Alignments

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SEQ. ID. NO. 44  A T G T T G C T G C T G C T G C T A C T G G C G C
SEQ. ID. NO. 42  A T G G C T T C C C C G C G G A G C T C C G G G C

SEQ. ID. NO. 44  C A C T C T T C C T C C G C C C C C C G G G C G C
SEQ. ID. NO. 42  A G C C C G G G C C G C C G C C G C C G C C G C C

SEQ. ID. NO. 44  G G G C G G G G C G C A G A C C C C C A A C G C C
SEQ. ID. NO. 42  A C C G C C G C C C G C G C G C C T G C T A C T G

SEQ. ID. NO. 44  A C C T C A G A A G G T T G C C A G A T C A T A C
SEQ. ID. NO. 42  C T A C T G C T G C T G C C G C T G C T G C T G C

SEQ. ID. NO. 44  A C C C G C C C T G G G A A G G G G G C A T C A G
SEQ. ID. NO. 42  C T C T G G C G C C C G G G G C C T G G G G C T G

SEQ. ID. NO. 44  G T A C C G G G G C C T G A C T C G G G A C C A G
SEQ. ID. NO. 42  G G C G C G G G G C G C C C C C C G G C C G C C G

SEQ. ID. NO. 44  G T G A A G G C T A T C A A C T T C C T G C C A G
SEQ. ID. NO. 42  C C C A G C A G C C C G C C G C T C T C C A T C A

SEQ. ID. NO. 44  T G G A C T A T G A G A T T G A G T A T G T G T G
SEQ. ID. NO. 42  T G G G C C T C A T G C C G C T C A C C A A G G A

SEQ. ID. NO. 44  C C G G G G G G A G C G C G A G G T G G T G G G G
SEQ. ID. NO. 42  G G T G G C C A A G G G C A G C A T C G G G C G C

SEQ. ID. NO. 44  C C C A A G G T C C G C A A G T G C C T G G C C A
SEQ. ID. NO. 42  G G T G T G C T C C C C G C C G T G G A A C T G G

SEQ. ID. NO. 44  A C G G C T C C T G G A C A G A T A T G G A C A C
SEQ. ID. NO. 42  C C A T C G A G C A G A T C C G C A A C G A G T C

SEQ. ID. NO. 44  A C C C A G C C G C T G T G T C C G A A T C T G C
SEQ. ID. NO. 42  A C T C C T G C G C C C T T A C T T C C T C G A C

```

Figure 13a

SEQ. ID. NO. 44 T C C A A G T C T T A T T T G A C C C T G G A A A
SEQ. ID. NO. 42 C T G C G G C T C T A T G A C A C G G A G T G C G

SEQ. ID. NO. 44 A T G G G A A G G T T T T C C T G A C G G G T G G
SEQ. ID. NO. 42 A C A A C G C A A A A G G G T T G A A A G C C T T

SEQ. ID. NO. 44 G G A C C T C C C A G C T C T G G A C G G A G C C
SEQ. ID. NO. 42 C T A C G A T G C A A T A A A A T A C G G G C C G

SEQ. ID. NO. 44 C G G G T G G A T T T C C G G T G T G A C C C C G
SEQ. ID. NO. 42 A A C C A C T T G A T G G T G T T T G G A G G C G

SEQ. ID. NO. 44 A C T T C C A T C T G G T G G G C A G C T C C C G
SEQ. ID. NO. 42 T C T G T C C A T C C G T C A C A T C C A T C A T

SEQ. ID. NO. 44 G A G C A T C T G T A G T C A G G G C C A G T G G
SEQ. ID. NO. 42 T G C A G A G T C C C T C C A A G G C T G G A A T

SEQ. ID. NO. 44 A G C A C C C C C A A G C C C C A C T G C C A G G
SEQ. ID. NO. 42 C T G G T G C A G C T T T C T T T T G C T G C A A

SEQ. ID. NO. 44 T G A A T C G A A C G C C A C A C T C A G A A C G
SEQ. ID. NO. 42 C C A C G C C T G T T C T A G C C G A T A A G A A

SEQ. ID. NO. 44 G C G C G C A G T G T A C A T C G G G G C A C T G
SEQ. ID. NO. 42 A A A A T A C C C T T A T T T C T T T C G G A C C

SEQ. ID. NO. 44 T T T C C C A T G A G C G G G G G C T G G C C A G
SEQ. ID. NO. 42 G T C C C A T C A G A C A A T G C G G T G A A T C

SEQ. ID. NO. 44 G G G G C C A G G C C T G C C A G C C C G C G G T
SEQ. ID. NO. 42 C A G C C A T T C T G A A G T T G C T C A A G C A

SEQ. ID. NO. 44 G G A G A T G G C G C T G G A G G A C G T G A A T
SEQ. ID. NO. 42 C T A C C A G T G G A A G C G C G T G G G C A C G

SEQ. ID. NO. 44 A G C C G C A G G G A C A T C C T G C C G G A C T
SEQ. ID. NO. 42 C T G A C G C A A G A C G T T C A G A G G T T C T

Figure 13b

SEQ. ID. NO. 44 A T G A G C T C A A G C T C A T C C A C C A C G A
SEQ. ID. NO. 42 C T G A G G T G C G G A A T G A C C T G A C T G G

SEQ. ID. NO. 44 C A G C A A G T G T G A T C C A G G C C A A G C C
SEQ. ID. NO. 42 A G T T C T G T A T G G C G A G G A C A T T G A G

SEQ. ID. NO. 44 A C C A A G T A C C T A T A T G A G C T G C T C T
SEQ. ID. NO. 42 A T T T C A G A C A C C G A G A G C T T C T C C A

SEQ. ID. NO. 44 A C A A C G A C C C T A T C A A G A T C A T C C T
SEQ. ID. NO. 42 A C G A T C C C T G T A C C A G T G T C A A A A A

SEQ. ID. NO. 44 T A T G C C T G G C T G C A G C T C T G T C T C C
SEQ. ID. NO. 42 G C T G A A G G G G A A T G A T G T G C G G A T C

SEQ. ID. NO. 44 A C G C T G G T G G C T G A G G C T G C T A G G A
SEQ. ID. NO. 42 A T C C T T G G C C A G T T T G A C C A G A A T A

SEQ. ID. NO. 44 T G T G G A A C C T C A T T G T G C T T T C C T A
SEQ. ID. NO. 42 T G G C A G C A A A A G T G T T C T G T T G T G C

SEQ. ID. NO. 44 T G G C T C C A G C T C A C C A G C C C T G T C A
SEQ. ID. NO. 42 A T A C G A G G A G A A C A T G T A T G G T A G T

SEQ. ID. NO. 44 A A C C G G C A G C G T T T C C C C A C T T T C T
SEQ. ID. NO. 42 A A A T A T C A G T G G A T C A T T C C G G G C T

SEQ. ID. NO. 44 T C C G A A C G C A C C C A T C A G C C A C A C T
SEQ. ID. NO. 42 G G T A C G A G C C T T C T T G G T G G G A G C A

SEQ. ID. NO. 44 C C A C A A C C C T A C C C G C G T G A A A C T C
SEQ. ID. NO. 42 G G T G C A C A C G G A A G C C A A C T C A T C C

SEQ. ID. NO. 44 T T T G A A A A G T G G G G C T G G A A G A A G A
SEQ. ID. NO. 42 C G C T G C C T C C G G A A G A A T C T G C T T G

SEQ. ID. NO. 44 T T G C T A C C A T C C A G C A G A C C A C T G A
SEQ. ID. NO. 42 C T G C C A T G G A G G G C T A C A T T G G C G T

Figure 13c

SEQ. ID. NO. 44 G G T C T T C A C T T C G A C T C T G G A C G A C
SEQ. ID. NO. 42 G G A T T T C G A G C C C C T G A G C T C C A A G

SEQ. ID. NO. 44 C T G G A G G A A C G A G T G A A G G A G G C T G
SEQ. ID. NO. 42 C A G A T C A A G A C C A T C T C A G G A A A G A

SEQ. ID. NO. 44 G A A T T G A G A T T A C T T T C C G C C A G A G
SEQ. ID. NO. 42 C T C C A C A G C A G T A T G A G A G A G A G T A

SEQ. ID. NO. 44 T T T C T T C T C A G A T C C A G C T G T G C C C
SEQ. ID. NO. 42 C A A C A A C A A G C G G T C A G G C G T G G G G

SEQ. ID. NO. 44 G T C A A A A A C C T G A A G C G C C A G G A T G
SEQ. ID. NO. 42 C C C A G C A A G T T C C A C G G G T A C G C C T

SEQ. ID. NO. 44 C C C G A A T C A T C G T G G G A C T T T T C T A
SEQ. ID. NO. 42 A C G A T G G C A T C T G G G T C A T C G C C A A

SEQ. ID. NO. 44 T G A G A C T G A A G C C C G G A A A G T T T T T
SEQ. ID. NO. 42 G A C A C T G C A G A G G G C C A T G G A G A C A

SEQ. ID. NO. 44 T G T G A G G T G T A C A A G G A G C G T C T C T
SEQ. ID. NO. 42 C T G C A T G C C A G C A G C C G G C A C C A G C

SEQ. ID. NO. 44 T T G G G A A G A A G T A C G T C T G G T T C C T
SEQ. ID. NO. 42 G G A T C C A G G A C T T C A A C T A C A C G G A

SEQ. ID. NO. 44 C A T T G G G T G G T A T G C T G A C A A T T G G
SEQ. ID. NO. 42 C C A C A C G C T G G G C A G G A T C A T C C T C

SEQ. ID. NO. 44 T T C A A G A T C T A C G A C C C T T C T A T C A
SEQ. ID. NO. 42 A A T G C C A T G A A C G A G A C C A A C T T C T

SEQ. ID. NO. 44 A C T G C A C A G T G G A T G A G A T G A C T G A
SEQ. ID. NO. 42 T C G G G G T C A C G G G T C A A G T T G T A T T

SEQ. ID. NO. 44 G G C G G T G G A G G G C C A C A T C A C A A C T
SEQ. ID. NO. 42 C C G G A A T G G G G A G A G A A T G G G G A C C

Figure 13d

SEQ. ID. NO. 44 G A G A T T G T C A T G C T G A A T C C T G C C A
SEQ. ID. NO. 42 A T T A A A T T T A C T C A A T T T C A A G A C A

SEQ. ID. NO. 44 A T A C C C G C A G C A T T T C C A A C A T G A C
SEQ. ID. NO. 42 G C A G G G A G G T G A A G G T G G G A G A G T A

SEQ. ID. NO. 44 A T C C C A G G A A T T T G T G G A G A A A C T A
SEQ. ID. NO. 42 C A A C G C T G T G G C C G A C A C A C T G G A G

SEQ. ID. NO. 44 A C C A A G C G A C T G A A A A G A C A C C C T G
SEQ. ID. NO. 42 A T C A T C A A T G A C A C C A T C A G G T T C C

SEQ. ID. NO. 44 A G G A G A C A G G A G G C T T C C A G G A G G C
SEQ. ID. NO. 42 A A G G A T C C G A A C C A C C A A A A G A C A A

SEQ. ID. NO. 44 A C C G C T G G C C T A T G A T G C C A T C T G G
SEQ. ID. NO. 42 G A C C A T C A T C C T G G A G C A G C T G C G G

SEQ. ID. NO. 44 G C C T T G G C A C T G G C C C T G A A C A A G A
SEQ. ID. NO. 42 A A G A T C T C C C T A C C T C T C T A C A G C A

SEQ. ID. NO. 44 C A T C T G G A G G A G G C G G C C G T T C T G G
SEQ. ID. NO. 42 T C C T C T C T G C C C T C A C C A T C C T C G G

SEQ. ID. NO. 44 T G T G C G C C T G G A G G A C T T C A A C T A C
SEQ. ID. NO. 42 G A T G A T C A T G G C C A G T G C T T T T C T C

SEQ. ID. NO. 44 A A C A A C C A G A C C A T T A C C G A C C A A A
SEQ. ID. NO. 42 T T C T T C A A C A T C A A G A A C C G G A A T C

SEQ. ID. NO. 44 T C T A C C G G G C A A T G A A C T C T T C G T C
SEQ. ID. NO. 42 A G A A G C T C A T A A A G A T G T C G A G T C C

SEQ. ID. NO. 44 C T T T G A G G G T G T C T C T G G C C A T G T G
SEQ. ID. NO. 42 A T A C A T G A A C A A C C T T A T C A T C C T T

SEQ. ID. NO. 44 G T G T T T G A T G C C A G C G G C T C T C G G A
SEQ. ID. NO. 42 G G A G G G A T G C T C T C C T A T G C T T C C A

Figure 13e

SEQ. ID. NO. 44 T G G C A T G G A C G C T T A T C G A G C A G C T
SEQ. ID. NO. 42 T A T T T C T C T T T G G C C T T G A T G G A T C

SEQ. ID. NO. 44 T C A G G G T G G C A G C T A C A A G A A G A T T
SEQ. ID. NO. 42 C T T T G T C T C T G A A A A G A C C T T T G A A

SEQ. ID. NO. 44 G G C T A C T A T G A C A G C A C C A A G G A T G
SEQ. ID. NO. 42 A C A C T T T G C A C C G T C A G G A C C T G G A

SEQ. ID. NO. 44 A T C T T T C C T G G T C C A A A A C A G A T A A
SEQ. ID. NO. 42 T T C T C A C C G T G G G C T A C A C G A C C G C

SEQ. ID. NO. 44 A T G G A T T G G A G G G T C C C C C C C A G C T
SEQ. ID. NO. 42 T T T T G G G G C C A T G T T T G C A A A G A C C

SEQ. ID. NO. 44 G A C C A G A C C C T G G T C A T C A A G A C A T
SEQ. ID. NO. 42 T G G A G A G T C C A C G C C A T C T T C A A A A

SEQ. ID. NO. 44 T C C G C T T C C T G T C A C A G A A A C T C T T
SEQ. ID. NO. 42 A T G T G A A A A T G A A G A A G A A G A T C A T

SEQ. ID. NO. 44 T A T C T C C G T C T C A G T T C T C T C C A G C
SEQ. ID. NO. 42 C A A G G A C C A G A A A C T G C T T G T G A T C

SEQ. ID. NO. 44 C T G G G C A T T G T C C T A G C T G T T G T C T
SEQ. ID. NO. 42 G T G G G G G G C A T G C T G C T G A T C G A C C

SEQ. ID. NO. 44 G T C T G T C C T T T A A C A T C T A C A A C T C
SEQ. ID. NO. 42 T G T G T A T C C T G A T C T G C T G G C A G G C

SEQ. ID. NO. 44 A C A T G T C C G T T A T A T C C A G A A C T C A
SEQ. ID. NO. 42 T G T G G A C C C C C T G C G A A G G A C A G T G

SEQ. ID. NO. 44 C A G C C C A A C C T G A A C A A C C T G A C T G
SEQ. ID. NO. 42 G A G A A G T A C A G C A T G G A G C C G G A C C

SEQ. ID. NO. 44 C T G T G G G C T G C T C A C T G G C T T T A G C
SEQ. ID. NO. 42 C A G C A G G A C G G G A T A T C T C C A T C C G

Figure 13f

SEQ. ID. NO. 44 T G C T G T C T T C C C C C T G G G G C T C G A T
SEQ. ID. NO. 42 C C C T C T C C T G G A G C A C T G T G A G A A C

SEQ. ID. NO. 44 G G T T A C C A C A T T G G G A G G A A C C A G T
SEQ. ID. NO. 42 A C C C A T A T G A C C A T C T G G C T T G G C A

SEQ. ID. NO. 44 T T C C T T T C G T C T G C C A G G C C C G C C T
SEQ. ID. NO. 42 T C G T C T A T G C C T A C A A G G G A C T T C T

SEQ. ID. NO. 44 C T G G C T C C T G G G C C T G G G C T T T A G T
SEQ. ID. NO. 42 C A T G T T G T T C G G T T G T T T C T T A G C T

SEQ. ID. NO. 44 C T G G G C T A C G G T T C C A T G T T C A C C A
SEQ. ID. NO. 42 T G G G A G A C C C G C A A C G T C A G C A T C C

SEQ. ID. NO. 44 A G A T T T G G T G G G T C C A C A C G G T C T T
SEQ. ID. NO. 42 C C G C A C T C A A C G A C A G C A A G T A C A T

SEQ. ID. NO. 44 C A C A A A G A A G G A A G A A A A G A A G G A G
SEQ. ID. NO. 42 C G G G A T G A G T G T C T A C A A C G T G G G G

SEQ. ID. NO. 44 T G G A G G A A G A C T C T G G A A C C C T G G A
SEQ. ID. NO. 42 A T C A T G T G C A T C A T C G G G G C C G C T G

SEQ. ID. NO. 44 A G C T G T A T G C C A C A G T G G G C C T G C T
SEQ. ID. NO. 42 T C T C C T T C C T G A C C C G G G A C C A G C C

SEQ. ID. NO. 44 G G T G G G C A T G G A T G T C C T C A C T C T C
SEQ. ID. NO. 42 C A A T G T G C A G T T C T G C A T C G T G G C T

SEQ. ID. NO. 44 G C C A T C T G G C A G A T C G T G G A C C C T C
SEQ. ID. NO. 42 C T G G T C A T C A T C T T C T G C A G C A C C A

SEQ. ID. NO. 44 T G C A C C G G A C C A T T G A G A C A T T T G C
SEQ. ID. NO. 42 T C A C C C T C T G C C T G G T A T T C G T G C C

SEQ. ID. NO. 44 C A A G G A G G A A C C T A A G G A A G A T A T T
SEQ. ID. NO. 42 G A A G C T C A T C A C C C T G A G A A C A A A C

Figure 13g

SEQ. ID. NO. 44 G A C G T C T C T A T T C T G C C C C A G C T G G
SEQ. ID. NO. 42 C C A G A T G C A G C A A C G C A G A A C A G G C

SEQ. ID. NO. 44 A G C A T T G C A G C T C C A G G A A G A T G A A
SEQ. ID. NO. 42 G A T T C C A G T T C A C T C A G A A T C A G A A

SEQ. ID. NO. 44 T A C A T G G C T T G G C A T T T T C T A T G G T
SEQ. ID. NO. 42 G A A A G A A G A T T C T A A A A C G T C C A C C

SEQ. ID. NO. 44 T A C A A G G G G C T G C T G C T G C T G C T G G
SEQ. ID. NO. 42 T C G G T C A C C A G T G T G A A C C A A G C C A

SEQ. ID. NO. 44 G A A T C T T C C T T G C T T A T G A G A C C A A
SEQ. ID. NO. 42 G C A C A T C C C G C C T G G A G G G C C T A C A

SEQ. ID. NO. 44 G A G T G T G T C C A C T G A G A A G A T C A A T
SEQ. ID. NO. 42 G T C A G A A A A C C A T C G C C T G C G A A T G

SEQ. ID. NO. 44 G A T C A C C G G G C T G T G G G C A T G G C T A
SEQ. ID. NO. 42 A A G A T C A C A G A G C T G G A T A A A G A C T

SEQ. ID. NO. 44 T C T A C A A T G T G G C A G T C C T G T G C C T
SEQ. ID. NO. 42 T G G A A G A G G T C A C C A T G C A G C T G C A

SEQ. ID. NO. 44 C A T C A C T G C T C C T G T C A C C A T G A T T
SEQ. ID. NO. 42 G G A C A C A C C A G A A A A G A C C A C C T A C

SEQ. ID. NO. 44 C T G T C C A G C C A G C A G G A T G C A G C C T
SEQ. ID. NO. 42 A T T A A A C A G A A C C A C T A C C A A G A G C

SEQ. ID. NO. 44 T T G C C T T T G C C T C T C T T G C C A T A G T
SEQ. ID. NO. 42 T C A A T G A C A T C C T C A A C C T G G G A A A

SEQ. ID. NO. 44 T T T C T C C T C C T A T A T C A C T C T T G T T
SEQ. ID. NO. 42 C T T C A C T G A G A G C A C A G A T G G A G G A

SEQ. ID. NO. 44 G T G C T C T T T G T G C C C A A G A T G C G C A
SEQ. ID. NO. 42 A A G G C C A T T T T A A A A A A T C A C C T C G

Figure 13h

SEQ. ID. NO. 44 G G C T G A T C A C C C G A G G G G A A T G G C A
SEQ. ID. NO. 42 A T C A A A A T C C C C A G C T A C A G T G G A A

SEQ. ID. NO. 44 G T C G G A G G C G C A G G A C A C C A T G A A G
SEQ. ID. NO. 42 C A C A A C A G A G C C C T C T C G A A C A T G C

SEQ. ID. NO. 44 A C A G G G T C A T C G A C C A A C A A C A A C G
SEQ. ID. NO. 42 A A A G A T C C T A T A G A A G A T A T A A A C T

SEQ. ID. NO. 44 A G G A G G A G A A G T C C C G G C T G T T G G A
SEQ. ID. NO. 42 C T C C A G A A C A C A T C C A G C G T C G G C T

SEQ. ID. NO. 44 G A A G G A G A A C C G T G A A C T G G A A A A G
SEQ. ID. NO. 42 G T C C C T C C A G C T C C C C A T C C T C C A C

SEQ. ID. NO. 44 A T C A T T G C T G A G A A A G A G G A G C G T G
SEQ. ID. NO. 42 C A C G C C T A C C T C C C A T C C A T C G G A G

SEQ. ID. NO. 44 T C T C T G A A C T G C G C C A T C A A C T C C A
SEQ. ID. NO. 42 G C G T G G A C G C C A G C T G T G T C A G C C C

SEQ. ID. NO. 44 G T C T C G G C A G C A G C T C C G C T C C C G G
SEQ. ID. NO. 42 C T G C G T C A G C C C C A C C G C C A G C C C C

SEQ. ID. NO. 44 C G C C A C C C A C C G A C A C C C C C A G A A C
SEQ. ID. NO. 42 C G C C A C A G A C A T G T G C C A C C C T C C T

SEQ. ID. NO. 44 C C T C T G G G G G C C T G C C C A G G G G A C C
SEQ. ID. NO. 42 T C C G A G T C A T G G T C T C G G G C C T G G C

SEQ. ID. NO. 44 C C C T G A G C C C C C C G A C C G G C T T A G C
SEQ. ID. NO. 42 G G C C G C C A T G A C T C T G G A G T C C A T C

SEQ. ID. NO. 44 T G T G A T G G G A G T C G A G T G C A T T T G C
SEQ. ID. NO. 42 A T G G C G T G C T G C C T G A G C G A G G A G G

SEQ. ID. NO. 44 T T T A T A A G G C G G C C G C C A T G A C T C T
SEQ. ID. NO. 42 C C A A G G A A G C C C G G C G G A T C A A C G A

Figure 13i

SEQ. ID. NO. 44 G G A G T C C A T C A T G G C G T G C T G C C T G
 SEQ. ID. NO. 42 C G A G A T C G A G C G G C A G C T C C G C A G G

SEQ. ID. NO. 44 A G C G A G G A G G C C A A G G A A G C C C G G C
 SEQ. ID. NO. 42 G A C A A G C G G G A C G C C C G C C G G G A G C

SEQ. ID. NO. 44 G G A T C A A C G A C G A G A T C G A G C G G C A
 SEQ. ID. NO. 42 T C A A G C T G C T G C T G C T C G G G A C A G G

SEQ. ID. NO. 44 G C T C C G C A G G G A C A A G C G G G A C G C C
 SEQ. ID. NO. 42 A G A G A G T G G C A A G A G T A C G T T T A T C

SEQ. ID. NO. 44 C G C C G G G A G C T C A A G C T G C T G C T G C
 SEQ. ID. NO. 42 A A G C A G A T G A G A A T C A T C C A T G G G T

SEQ. ID. NO. 44 T C G G G A C A G G A G A G A G T G G C A A G A G
 SEQ. ID. NO. 42 C A G G A T A C T C T G A T G A A G A T A A A A G

SEQ. ID. NO. 44 T A C G T T T A T C A A G C A G A T G A G A A T C
 SEQ. ID. NO. 42 G G G C T T C A C C A A G C T G G T G T A T C A G

SEQ. ID. NO. 44 A T C C A T G G G T C A G G A T A C T C T G A T G
 SEQ. ID. NO. 42 A A C A T C T T C A C G G C C A T G C A G G C C A

SEQ. ID. NO. 44 A A G A T A A A A G G G G C T T C A C C A A G C T
 SEQ. ID. NO. 42 T G A T C A G A G C C A T G G A C A C A C T C A A

SEQ. ID. NO. 44 G G T G T A T C A G A A C A T C T T C A C G G C C
 SEQ. ID. NO. 42 G A T C C C A T A C A A G T A T G A G C A C A A T

SEQ. ID. NO. 44 A T G C A G G C C A T G A T C A G A G C C A T G G
 SEQ. ID. NO. 42 A A G G C T C A T G C A C A A T T A G T T C G A G

SEQ. ID. NO. 44 A C A C A C T C A A G A T C C C A T A C A A G T A
 SEQ. ID. NO. 42 A A G T T G A T G T G G A G A A G G T G T C T G C

SEQ. ID. NO. 44 T G A G C A C A A T A A G G C T C A T G C A C A A
 SEQ. ID. NO. 42 T T T T G A G A A T C C A T A T G T A G A T G C A

Figure 13j

SEQ. ID. NO. 44 T T A G T T C G A G A A G T T G A T G T G G A G A
SEQ. ID. NO. 42 A T A A A G A G T T T A T G G A A T G A T C C T G

SEQ. ID. NO. 44 A G G T G T C T G C T T T T G A G A A T C C A T A
SEQ. ID. NO. 42 G A A T C C A G G A A T G C T A T G A T A G A C G

SEQ. ID. NO. 44 T G T A G A T G C A A T A A A G A G T T T A T G G
SEQ. ID. NO. 42 A C G A G A A T A T C A A T T A T C T G A C T C T

SEQ. ID. NO. 44 A A T G A T C C T G G A A T C C A G G A A T G C T
SEQ. ID. NO. 42 A C C A A A T A C T A T C T T A A T G A C T T G G

SEQ. ID. NO. 44 A T G A T A G A C G A C G A G A A T A T C A A T T
SEQ. ID. NO. 42 A C C G C G T A G C T G A C C C T G C C T A C C T

SEQ. ID. NO. 44 A T C T G A C T C T A C C A A A T A C T A T C T T
SEQ. ID. NO. 42 G C C T A C G C A A C A A G A T G T G C T T A G A

SEQ. ID. NO. 44 A A T G A C T T G G A C C G C G T A G C T G A C C
SEQ. ID. NO. 42 G T T C G A G T C C C C A C C A C A G G G A T C A

SEQ. ID. NO. 44 C T G C C T A C C T G C C T A C G C A A C A A G A
SEQ. ID. NO. 42 T C G A A T A C C C C T T T G A C T T A C A A A G

SEQ. ID. NO. 44 T G T G C T T A G A G T T C G A G T C C C C A C C
SEQ. ID. NO. 42 T G T C A T T T T C A G A A T G G T C G A T G T A

SEQ. ID. NO. 44 A C A G G G A T C A T C G A A T A C C C C T T T G
SEQ. ID. NO. 42 G G G G G C C A A A G G T C A G A G A G A A G A A

SEQ. ID. NO. 44 A C T T A C A A A G T G T C A T T T T C A G A A T
SEQ. ID. NO. 42 A A T G G A T A C A C T G C T T T G A A A A T G T

SEQ. ID. NO. 44 G G T C G A T G T A G G G G G C C A A A G G T C A
SEQ. ID. NO. 42 C A C C T C T A T C A T G T T T C T A G T A G C G

SEQ. ID. NO. 44 G A G A G A A G A A A A T G G A T A C A C T G C T
SEQ. ID. NO. 42 C T T A G T G A A T A T G A T C A A G T T C T G G

Figure 13k

SEQ. ID. NO. 44 T T G A A A A T G T C A C C T C T A T C A T G T T
SEQ. ID. NO. 42 T G G A G T C A G A C A A T G A G A A C C G A A T

SEQ. ID. NO. 44 T C T A G T A G C G C T T A G T G A A T A T G A T
SEQ. ID. NO. 42 G G A G G A A A G C A A G G C T C T C T T T A G A

SEQ. ID. NO. 44 C A A G T T C T C G T G G A G T C A G A C A A T G
SEQ. ID. NO. 42 A C A A T T A T C A C A T A C C C C T G G T T C C

SEQ. ID. NO. 44 A G A A C C G A A T G G A G G A A A G C A A G G C
SEQ. ID. NO. 42 A G A A C T C C T C G G T T A T T C T G T T C T T

SEQ. ID. NO. 44 T C T C T T T A G A A C A A T T A T C A C A T A C
SEQ. ID. NO. 42 A A A C A A G A A A G A T C T T C T A G A G G A G

SEQ. ID. NO. 44 C C C T G G T T C C A G A A C T C C T C G G T T A
SEQ. ID. NO. 42 A A A A T C A T G T A T T C C C A T C T A G T C G

SEQ. ID. NO. 44 T T C T G T T C T T A A A C A A G A A A G A T C T
SEQ. ID. NO. 42 A C T A C T T C C C A G A A T A T G A T G G A C C

SEQ. ID. NO. 44 T C T A G A G G A G A A A A T C A T G T A T T C C
SEQ. ID. NO. 42 C C A G A G A G A T G C C C A G G C A G C C C G A

SEQ. ID. NO. 44 C A T C T A G T C G A C T A C T T C C C A G A A T
SEQ. ID. NO. 42 G A A T T C A T T C T G A A G A T G T T C G T G G

SEQ. ID. NO. 44 A T G A T G G A C C C C A G A G A G A T G C C C A
SEQ. ID. NO. 42 A C C T G A A C C C A G A C A G T G A C A A A A T

SEQ. ID. NO. 44 G G C A G C C C G A G A A T T C A T T C T G A A G
SEQ. ID. NO. 42 T A A C T A C T C C C A C T T C A C G T G C G C C

SEQ. ID. NO. 44 A T G T T C G T G G A C C T G A A C C C A G A C A
SEQ. ID. NO. 42 A C A G A C A C C G A G A A T A T C C G C T T T G

SEQ. ID. NO. 44 G T G A C A A A A T T A T C T A C T C C C A C T T
SEQ. ID. NO. 42 T C T T T G C T G C C G T C A A G G A C A C C A T

Figure 13L

SEQ. ID. NO. 44 C A C G T G C G C C A C A G A C A C C G A G A A T
SEQ. ID. NO. 42 C C T C C A G T T G A A C C T G A A G G G C T G C

SEQ. ID. NO. 44 A T C C G C T T T G T C T T T G C T G C C G T C A
SEQ. ID. NO. 42 G G T C T G T A C

SEQ. ID. NO. 44 A G G A C A C C A T C C T C C A G T T G A A C C T
SEQ. ID. NO. 42

SEQ. ID. NO. 44 G A A G G G C T G C G G T C T G T A C
SEQ. ID. NO. 42

Figure 13M

ClustalW Formatted Alignments

SEQ. ID. NO. 45 M L L L L L L A P L F L R P P G A G G A Q T P N A
SEQ. ID. NO. 43 M A S P R S S G Q P G P P P P P P P P A R L L L

SEQ. ID. NO. 45 T S E G C Q I I H P P W E G G I R Y R G L T R D Q
SEQ. ID. NO. 43 L L L L P L L L P L A P G A W G W A R G A P R P P

SEQ. ID. NO. 45 V K A I N F L P V D Y E I E Y V C R G E R E V V G
SEQ. ID. NO. 43 P S S P P L S I M G L M P L T K E V A K G S I G R

SEQ. ID. NO. 45 P K V R K C L A N G S W T D M D T P S R C V R I C
SEQ. ID. NO. 43 G V L P A V E L A I E Q I R N E S L L R P Y F L D

SEQ. ID. NO. 45 S K S Y L T L E N G K V F L T G G D L P A L D G A
SEQ. ID. NO. 43 L R L Y D T E C D N A K G L K A F Y D A I K Y G P

SEQ. ID. NO. 45 R V D F R C D P D F H L V G S S R S I C S Q G Q W
SEQ. ID. NO. 43 N H L M V F G G V C P S V T S I I A E S L Q G W N

SEQ. ID. NO. 45 S T P K P H C Q V N R T P H S E R R A V Y I G A L
SEQ. ID. NO. 43 L V Q L S F A A T T P V L A D K K K Y P Y F F R T

SEQ. ID. NO. 45 F P M S G G W P G G Q A C Q P A V E M A L E D V N
SEQ. ID. NO. 43 V P S D N A V N P A I L K L L K H Y Q W K R V G T

SEQ. ID. NO. 45 S R R D I L P D Y E L K L I H H D S K C D P G Q A
SEQ. ID. NO. 43 L T Q D V Q R F S E V R N D L T G V L Y G E D I E

SEQ. ID. NO. 45 T K Y L Y E L L Y N D P I K I I L M P G C S S V S
SEQ. ID. NO. 43 I S D T E S F S N D P C T S V K K L K G N D V R I

SEQ. ID. NO. 45 T L V A E A A R M W N L I V L S Y G S S S P A L S
SEQ. ID. NO. 43 I L G Q F D Q N M A A K V F C C A Y E E N M Y G S

SEQ. ID. NO. 45 N R Q R F P T F F R T H P S A T L H N P T R V K L
SEQ. ID. NO. 43 K Y Q W I I P G W Y E P S W W E Q V H T E A N S S

Figure 14a

SEQ. ID. NO. 45 F E K W G W K K I A T I Q Q T T E V F T S T L D D
SEQ. ID. NO. 43 R C L R K N L L A A M E G Y I G V D F E P L S S K

SEQ. ID. NO. 45 L E E R V K E A G I E I T F R Q S F F S D P A V P
SEQ. ID. NO. 43 Q I K T I S G K T P Q Q Y E R E Y N N K R S G V G

SEQ. ID. NO. 45 V K N L K R Q D A R I I V G L F Y E T E A R K V F
SEQ. ID. NO. 43 P S K F H G Y A Y D G I W V I A K T L Q R A M E T

SEQ. ID. NO. 45 C E V Y K E R L F G K K Y V W F L I G W Y A D N W
SEQ. ID. NO. 43 L H A S S R H Q R I Q D F N Y T D H T L G R I I L

SEQ. ID. NO. 45 F K I Y D P S I N C T V D E M T E A V E G H I T T
SEQ. ID. NO. 43 N A M N E T N F F G V T G Q V V F R N G E R M G T

SEQ. ID. NO. 45 E I V M L N P A N T R S I S N M T S Q E F V E K L
SEQ. ID. NO. 43 I K F T Q F Q D S R E V K V G E Y N A V A D T L E

SEQ. ID. NO. 45 T K R L K R H P E E T G G - F Q E A P L A Y D A I
SEQ. ID. NO. 43 I I N D T I R F Q G S E P P K D K T I I L E Q L R

SEQ. ID. NO. 45 W A L A L A L N K T S G G G G R S G V R L E D F N
SEQ. ID. NO. 43 K I S L P L Y S I L S A L T I L G M I M A S A F L

SEQ. ID. NO. 45 Y N N Q T I T D Q I Y R A M N S S S F E G V S G H
SEQ. ID. NO. 43 F F N I K N R N Q K L I K M S S P Y M N N L I I L

SEQ. ID. NO. 45 V V F D A S G S R M A W T L I E Q L Q G G S Y K K
SEQ. ID. NO. 43 G G M L S Y A S I F L F G L D G S F V S E K T F E

SEQ. ID. NO. 45 I G Y Y D S T K D D L S W S K T D K W I G G S P P
SEQ. ID. NO. 43 T L C T V R T W I L T V G Y T T A F G A M F A K T

SEQ. ID. NO. 45 A D Q T L V I K T F R F L S Q K L F I S V S V L S
SEQ. ID. NO. 43 W R V H A I F K N V K M K K K I I K D Q K L L V I

SEQ. ID. NO. 45 S L G I V L A V V C L S F N I Y N S H V R Y I Q N
SEQ. ID. NO. 43 V G G M L L I D L C I L I C W Q A V D P L R R T V

Figure 14b

SEQ. ID. NO. 45 S Q P N L N N L T A V G C S L A L A A V F P L G L
SEQ. ID. NO. 43 E K Y S M E P D P A G R D I S I R P L L E H C E N

SEQ. ID. NO. 45 D G Y H I G R N Q F P F V C Q A R L W L L G L G F
SEQ. ID. NO. 43 T H M T I W L G I V Y A Y K G L L M L F G C F L A

SEQ. ID. NO. 45 S L G Y G S M F T K I W W V H T V F T K K E E K K
SEQ. ID. NO. 43 W E T R N V S I P A L N D S K Y I G M S V Y N V G

SEQ. ID. NO. 45 E W R K T L E P W K L Y A T V G L L V G M D V L T
SEQ. ID. NO. 43 I M C I I G A A V S F L T R D Q P N V Q F C I V A

SEQ. ID. NO. 45 L A I W Q I V D P L H R T I E T F A K E E P K E D
SEQ. ID. NO. 43 L V I I F C S T I T L C L V F V P K L I T L R T N

SEQ. ID. NO. 45 I D V S I L P Q L E H C S S R K M N T W L G I F Y
SEQ. ID. NO. 43 P D A A T Q N R R F Q F T Q N Q K K E D S K T S T

SEQ. ID. NO. 45 G Y K G L L L L L G I F L A Y E T K S V S T E K I
SEQ. ID. NO. 43 S V T S V N Q A S T S R L E G L Q S E N H R L R M

SEQ. ID. NO. 45 N D H R A V G M A I Y N V A V L C L I T A P V T M
SEQ. ID. NO. 43 K I T E L D K D L E E V T M Q L Q D T P E K T T Y

SEQ. ID. NO. 45 I L S S Q Q D A A F A F A S L A I V F S S Y I T L
SEQ. ID. NO. 43 I K Q N H Y Q E L N D I L N L G N F T E S T D G G

SEQ. ID. NO. 45 V V L F V P K M R R L I T R G E W Q S E A Q D T M
SEQ. ID. NO. 43 K A I L K N H L D Q N P Q L Q W N T T E P S R T C

SEQ. ID. NO. 45 K T G S S T N N N E E E K S R L L E K E N R E L E
SEQ. ID. NO. 43 K D P I E D I N S P E H I Q R R L S L Q L P I L H

SEQ. ID. NO. 45 K I I A E K E E R V S E L R H Q L Q S R Q Q L R S
SEQ. ID. NO. 43 H A Y L P S I G G V D A S C V S P C V S P T A S P

SEQ. ID. NO. 45 R R H P P T P P E P S G G L P R G P P E P P D R L
SEQ. ID. NO. 43 R H R H V P P S F R V M V S G L A A A M T L E S I

Figure 14c

SEQ. ID. NO. 45 S C D G S R V H L L Y K A A A M T L E S I M A C C
SEQ. ID. NO. 43 M A C C L S E E A K E A R R I N D E I E R Q L R R

SEQ. ID. NO. 45 L S E E A K E A R R I N D E I E R Q L R R D K R D
SEQ. ID. NO. 43 D K R D A R R E L K L L L L G T G E S G K S T F I

SEQ. ID. NO. 45 A R R E L K L L L L G T G E S G K S T F I K Q M R
SEQ. ID. NO. 43 K Q M R I I H G S G Y S D E D K R G F T K L V Y Q

SEQ. ID. NO. 45 I I H G S G Y S D E D K R G F T K L V Y Q N I F T
SEQ. ID. NO. 43 N I F T A M Q A M I R A M D T L K I P Y K Y E H N

SEQ. ID. NO. 45 A M Q A M I R A M D T L K I P Y K Y E H N K A H A
SEQ. ID. NO. 43 K A H A Q L V R E V D V E K V S A F E N P Y V D A

SEQ. ID. NO. 45 Q L V R E V D V E K V S A F E N P Y V D A I K S L
SEQ. ID. NO. 43 I K S L W N D P G I Q E C Y D R R R E Y Q L S D S

SEQ. ID. NO. 45 W N D P G I Q E C Y D R R R E Y Q L S D S T K Y Y
SEQ. ID. NO. 43 T K Y Y L N D L D R V A D P A Y L P T Q Q D V L R

SEQ. ID. NO. 45 L N D L D R V A D P A Y L P T Q Q D V L R V R V P
SEQ. ID. NO. 43 V R V P T T G I I E Y P F D L Q S V I F R M V D V

SEQ. ID. NO. 45 T T G I I E Y P F D L Q S V I F R M V D V G G Q R
SEQ. ID. NO. 43 G G Q R S E R R K W I H C F E N V T S I M F L V A

SEQ. ID. NO. 45 S E R R K W I H C F E N V T S I M F L V A L S E Y
SEQ. ID. NO. 43 L S E Y D Q V L V E S D N E N R M E E S K A L F R

SEQ. ID. NO. 45 D Q V L V E S D N E N R M E E S K A L F R T I I T
SEQ. ID. NO. 43 T I I T Y P W F Q N S S V I L F L N K K D L L E E

SEQ. ID. NO. 45 Y P W F Q N S S V I L F L N K K D L L E E K I M Y
SEQ. ID. NO. 43 K I M Y S H L V D Y F P E Y D G P Q R D A Q A A R

SEQ. ID. NO. 45 S H L V D Y F P E Y D G P Q R D A Q A A R E F I L
SEQ. ID. NO. 43 E F I L K M F V D L N P D S D K I N Y S H F T C A

Figure 14d

SEQ. ID. NO. 45 K M F V D L N P D S D K I I Y S H F T C A T D T E
SEQ. ID. NO. 43 T D T E N I R F V F A A V K D T I L Q L N L K G C

SEQ. ID. NO. 45 N I R F V F A A V K D T I L Q L N L K G C G L Y
SEQ. ID. NO. 43 G L Y

Figure 14e

mGluR8//CaR*Gqi5

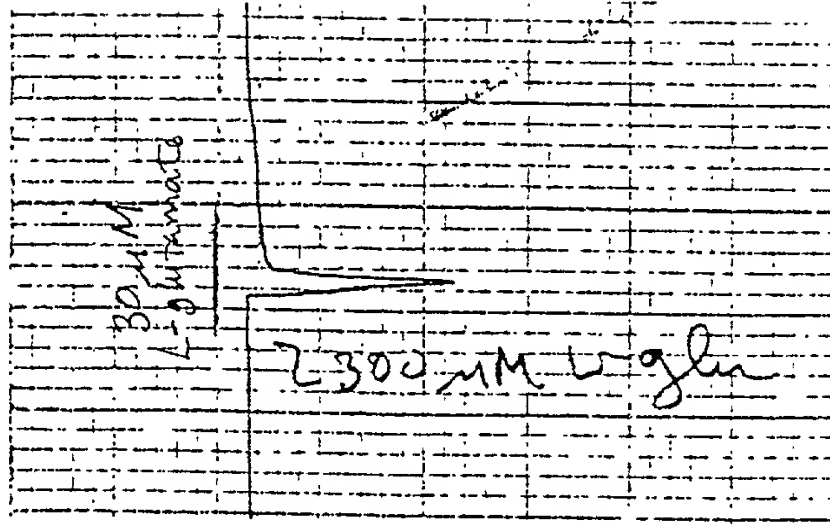
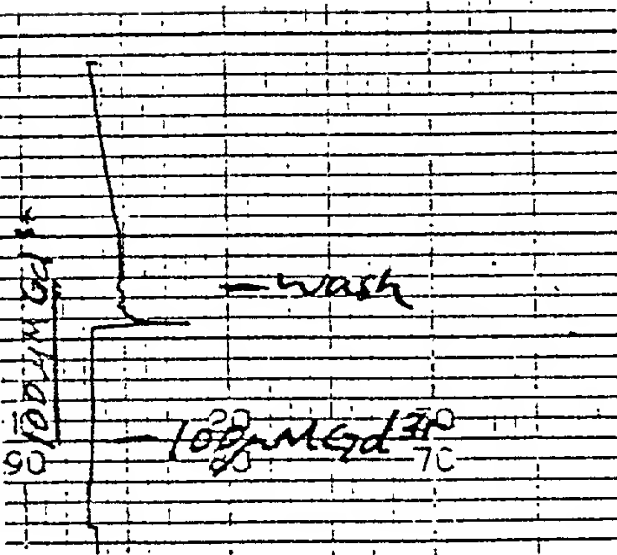


Figure 15

CaR/mGluR2*Gqi5



mGluR2//CaR*Gqi5

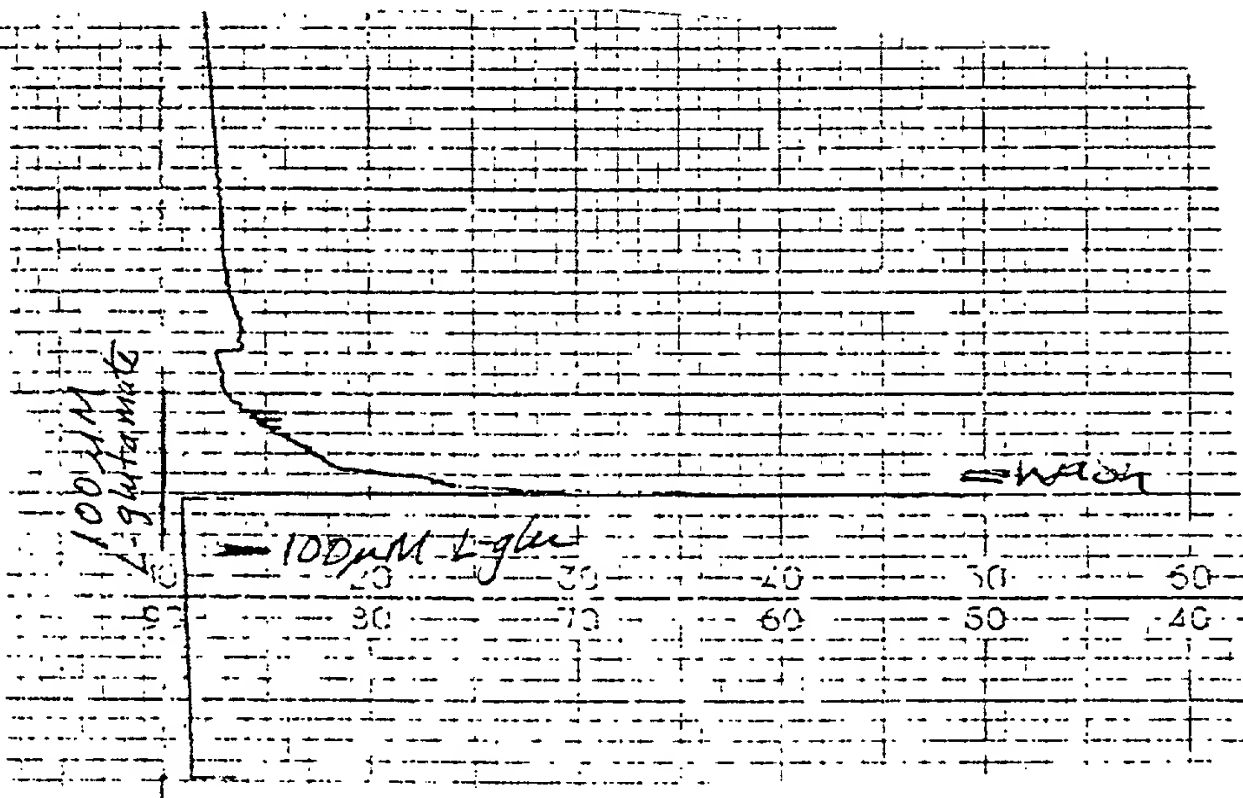


FIGURE 16A

SEQ. ID. NO. 48	M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R
SEQ. ID. NO. 49	M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R
SEQ. ID. NO. 50	M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R

SEQ. ID. NO. 48	T H S Q E Y A H S I R I D G D I T L G G L F P V H G R G S E
SEQ. ID. NO. 49	T H S Q E Y A H S I R I D G D I T L G G L F P V H G R G S E
SEQ. ID. NO. 50	T H S Q E Y A H S I R V D G D I I L G G L F P V H A K G E R

SEQ. ID. NO. 48	G K P C G E L K K E K G I H R L E A M L F A L D R I N N D P
SEQ. ID. NO. 49	G K P C G E L K K E K G I H R L E A M L F A L D R I N N D P
SEQ. ID. NO. 50	G V P C G E L K K E K G I H R L E A M L Y A I D Q I N K D P

SEQ. ID. NO. 48	D L L P N I T L G A R I L D T C S R D T H A L E Q S L T F V
SEQ. ID. NO. 49	D L L P N I T L G A R I L D T C S R D T H A L E Q S L T F V
SEQ. ID. NO. 50	D L L S N I T L G V R I L D T C S R D T Y A L E Q S L T F V

SEQ. ID. NO. 48	Q A L I E K D G T E V R C G S G G P P I I T K P E R V V G V
SEQ. ID. NO. 49	Q A L I E K D G T E V R C G S G G P P I I T K P E R V V G V
SEQ. ID. NO. 50	Q A L I E K D A S D V K C A N G D P P I F T K P D K I S G V

SEQ. ID. NO. 48	I G A S G S S V S I M V A N I L R L F K I P Q I S Y A S T A
SEQ. ID. NO. 49	I G A S G S S V S I M V A N I L R L F K I P Q I S Y A S T A
SEQ. ID. NO. 50	I G A A A S S V S I M V A N I L R L F K I P Q I S Y A S T A

SEQ. ID. NO. 48	P D L S D N S R Y D F F S R V V P S D T Y Q A Q A M V D I V
SEQ. ID. NO. 49	P D L S D N S R Y D F F S R V V P S D T Y Q A Q A M V D I V
SEQ. ID. NO. 50	P E L S D N T R Y D F F S R V V P P D S Y Q A Q A M V D I V

SEQ. ID. NO. 48	R A L K W N Y V S T V A S E G S Y G E S G V E A F I Q K S R
SEQ. ID. NO. 49	R A L K W N Y V S T V A S E G S Y G E S G V E A F I Q K S R
SEQ. ID. NO. 50	T A L G W N Y V S T L A S E G N Y G E S G V E A F T Q I S R

SEQ. ID. NO. 48	E D G G V C I A Q S V K I P R E P K A G E F D K I I R R L L
SEQ. ID. NO. 49	E D G G V C I A Q S V K I P R E P K A G E F D K I I R R L L
SEQ. ID. NO. 50	E I G G V C I A Q S Q K I P R E P R P G E F E K I I K R L L

FIGURE 16B

SEQ. ID. NO. 48 E T S N A R A V I I F A N E D D I R R V L E A A R R A N Q T
SEQ. ID. NO. 49 E T S N A R A V I I F A N E D D I R R V L E A A R R A N Q T
SEQ. ID. NO. 50 E T P N A R A V I M F A N E D D I R R I L E A A K K L N Q S

SEQ. ID. NO. 48 G H F F W M G S D S W G S K I A P V L H L E E V A E G A V T
SEQ. ID. NO. 49 G H F F W M G S D S W G S K I A P V L H L E E V A E G A V T
SEQ. ID. NO. 50 G H F L W I G S D S W G S K I A P V Y Q Q E E I A E G A V T

SEQ. ID. NO. 48 I L P K R M S V R G F D R Y F S S R T L D N N R R N I W F A
SEQ. ID. NO. 49 I L P K R M S V R G F D R Y F S S R T L D N N R R N I W F A
SEQ. ID. NO. 50 I L P K R A S I D G F D R Y F R S R T L A N N R R N V W F A

SEQ. ID. NO. 48 E F W E D N F H C K L S R H A L K K G S H V K K C T N R E R
SEQ. ID. NO. 49 E F W E D N F H C K L S R H A L K K G S H V K K C T N R E R
SEQ. ID. NO. 50 E F W E E N F G C K L G S H G K R N - S H I K K C T G L E R

SEQ. ID. NO. 48 I G Q D S A Y E Q E G K V Q F V I D A V Y A M G H A L H A M
SEQ. ID. NO. 49 I G Q D S A Y E Q E G K V Q F V I D A V Y A M G H A L H A M
SEQ. ID. NO. 50 I A R D S S Y E Q E G K V Q F V I D A V Y S M A Y A L H N M

SEQ. ID. NO. 48 H R D L C P G R V G L C P R M D P V D G T Q L L K Y I R N V
SEQ. ID. NO. 49 H R D L C P G R V G L C P R M D P V D G T Q L L K Y I R N V
SEQ. ID. NO. 50 H K D L C P G Y I G L C P R M S T I D G K E L L G Y I R A V

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SEQ. ID. NO. 49 N F S G I A G N P V T F N E N G D A P G R Y D I Y Q Y Q L R
SEQ. ID. NO. 50 N F N G S A G T P V T F N E N G D A P G R Y D I F Q Y Q I T

SEQ. ID. NO. 48 N D S A E Y K V I G S W T D H L H L R I E R M H W P G S G Q
SEQ. ID. NO. 49 N D S A E Y K V I G S W T D H L H L R I E R M H W P G S G Q
SEQ. ID. NO. 50 N K S T E Y K V I G H W T N Q L H L K V E D M Q W A H R E H

SEQ. ID. NO. 48 Q L P R S I C S L P C Q P G E R K K T V K G M P C C W H C E
SEQ. ID. NO. 49 Q L P R S I C S L P C Q P G E R K K T V K G M P C C W H C E
SEQ. ID. NO. 50 T H P A S V C S L P C K P G E R K K T V K G V P C C W H C E

SEQ. ID. NO. 48 P C T G Y Q Y Q V D R Y T C K T C P Y D M R P T E N R T G C
SEQ. ID. NO. 49 P C T G Y Q Y Q V D R Y T C K T C P Y D M R P T E N R T G C
SEQ. ID. NO. 50 R C E G Y N Y Q V D E L S C E L C P L D Q R P N M N R T G C

FIGURE 16C

SEQ. ID. NO. 48 R P I P I I K L E W G S P W A V L P L F L A V V G I A A T L
 SEQ. ID. NO. 49 R P I P I I K L E W G S P W A V L P L F L A V V G I A A T L
 SEQ. ID. NO. 50 Q L I P I I K L E W H S P W A V V P V F V A I L G I I A T T

SEQ. ID. NO. 48 F V V I T F V R Y N D T P I V K A S G R E L S Y V L L A G I
 SEQ. ID. NO. 49 F V V I T F V R Y N D T P I V K A S G R E L S Y V L L A G I
 SEQ. ID. NO. 50 F V I V T F V R Y N D T P I V R A S G R E L S Y V L L T G I

SEQ. ID. NO. 48 F L C Y A T T F L M I A E P D L G T C S L R R I F L G L G M
 SEQ. ID. NO. 49 F L C Y A T T F L M I A E P D L G T C S L R R I F L G L G M
 SEQ. ID. NO. 50 F L C Y S I T F L M I A A P D T I I C S F R R V F L G L G M

SEQ. ID. NO. 48 S I S Y A A L L T K T N R I Y R I F E Q G K R S V S A P R F
 SEQ. ID. NO. 49 S I S Y A A L L T K T N R I Y R I F E Q G K R S V S A P R F
 SEQ. ID. NO. 50 C F S Y A A L L T K T N R I H R I F E Q G K K S V T A P K F

SEQ. ID. NO. 48 I S P A S Q L A I T F S L I S L Q L L G I C V W F V V D P S
 SEQ. ID. NO. 49 I S P A S Q L A I T F S L I S L Q L L G I C V W F V V D P S
 SEQ. ID. NO. 50 I S P A S Q L V I T F S L I S V Q L L G V F V W F V V D P P

SEQ. ID. NO. 48 H S V V D F Q D Q R T L D P R F A R G V L K C D I S D L S L
 SEQ. ID. NO. 49 H S V V D F Q D Q R T L D P R F A R G V L K C D I S D L S L
 SEQ. ID. NO. 50 H I I I D Y G E Q R T L D P E K A R G V L K C D I S D L S L

SEQ. ID. NO. 48 I C L L G Y S M L L M V T C T V Y A I K T R G V P E T F N E
 SEQ. ID. NO. 49 I C L L G Y S M L L M V T C T V Y A I K T R G V P E T F N E
 SEQ. ID. NO. 50 I C S L G Y S I L L M V T C T V Y A I K T R G V P E T F N E

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 SEQ. ID. NO. 50 A K P I G F T M Y T T C I I W L A F I P I F F G T A Q S A E

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SEQ. ID. NO. 48 I I L F H P E Q N V P K R K R S L K A V V T A A T M S N K F
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 SEQ. ID. NO. 50 I I I F H P E Q N T I E E V R C S T A A H A F K V A A R A T

FIGURE 16D

SEQ. ID. NO. 48 T Q K G N F R P N G E A K S E L C E N L E A P A L A T K Q T
 SEQ. ID. NO. 49 L R R S N V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 50 L R R S N V S R K R S S S L G G S T G S T P S S S I S S K S

SEQ. ID. NO. 48 Y V T Y T N H A I
 SEQ. ID. NO. 49 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L
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SEQ. ID. NO. 48
 SEQ. ID. NO. 49 T L P Q Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S
 SEQ. ID. NO. 50 T L P Q Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S

SEQ. ID. NO. 48
 SEQ. ID. NO. 49 F D E P Q K N A M A H G N S T H Q N S L E A Q K S S D T L T
 SEQ. ID. NO. 50 F D E P Q K N A M A H G N S T H Q N S L E A Q K S S D T L T

SEQ. ID. NO. 48
 SEQ. ID. NO. 49 R H Q P L L P L Q C G E T D L D L T V Q E T G L Q G P V G G
 SEQ. ID. NO. 50 R H Q P L L P L Q C G E T D L D L T V Q E T G L Q G P V G G

SEQ. ID. NO. 48
 SEQ. ID. NO. 49 D Q R P E V E D P E E L S P A L V V S S S Q S F V I S G G G
 SEQ. ID. NO. 50 D Q R P E V E D P E E L S P A L V V S S S Q S F V I S G G G

SEQ. ID. NO. 48
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SEQ. ID. NO. 48
 SEQ. ID. NO. 49 A R R I N D E I E R Q L R R D K R D A R R E L K L L L L G T
 SEQ. ID. NO. 50 A R R I N D E I E R Q L R R D K R D A R R E L K L L L L G T

SEQ. ID. NO. 48
 SEQ. ID. NO. 49 G E S G K S T F I K Q M R I I H G S G Y S D E D K R G F T K
 SEQ. ID. NO. 50 G E S G K S T F I K Q M R I I H G S G Y S D E D K R G F T K

SEQ. ID. NO. 48
 SEQ. ID. NO. 49 L V Y Q N I F T A M Q A M I R A M D T L K I P Y K Y E H N K
 SEQ. ID. NO. 50 L V Y Q N I F T A M Q A M I R A M D T L K I P Y K Y E H N K

FIGURE 16E

SEQ. ID. NO. 48
SEQ. ID. NO. 49 A H A Q L V R E V D V E K V S A F E N P Y V D A I K S L W N
SEQ. ID. NO. 50 A H A Q L V R E V D V E K V S A F E N P Y V D A I K S L W N

SEQ. ID. NO. 48
SEQ. ID. NO. 49 D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R V
SEQ. ID. NO. 50 D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R V

SEQ. ID. NO. 48
SEQ. ID. NO. 49 A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q
SEQ. ID. NO. 50 A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q

SEQ. ID. NO. 48
SEQ. ID. NO. 49 S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M
SEQ. ID. NO. 50 S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M

SEQ. ID. NO. 48
SEQ. ID. NO. 49 F L V A L S E Y D Q V L V E S D N E N R M E E S K A L F R T
SEQ. ID. NO. 50 F L V A L S E Y D Q V L V E S D N E N R M E E S K A L F R T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 I I T Y P W F Q N S S V I L F L N K K D L L E E K I M Y S H
SEQ. ID. NO. 50 I I T Y P W F Q N S S V I L F L N K K D L L E E K I M Y S H

SEQ. ID. NO. 48
SEQ. ID. NO. 49 L V D Y F P E Y D G P Q R D A Q A A R E F I L K M F V D L N
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			20				25						30		
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		35					40					45			
Gln	Asp	Leu	Lys	Ser	Arg	Pro	Glu	Ser	Val	Glu	Cys	Ile	Arg	Tyr	Asn
	50					55					60				
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65					70					75				80	
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			85					90						95	
Ile	Phe	Asp	Thr	Cys	Asn	Thr	Val	Ser	Lys	Ala	Leu	Glu	Ala	Thr	Leu
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Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
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Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
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Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
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Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
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Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
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Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
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Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
 260 265 270

Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
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Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
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Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
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Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
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Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
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Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
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Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile

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Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser	435		440		445
Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu	450		455		460
Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp	465		470		475
Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu	485		490		495
Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn	500		505		510
Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile	515		520		525
Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg	530		535		540
Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr	545		550		555
Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu	565		570		575
Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn	580		585		590
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Thr Glu Pro Phe	610				

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Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
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 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60
 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
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 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
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 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
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 Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
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 Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile
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 Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn
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 Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe
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 Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val
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 Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp
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 Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln
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 Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile
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 Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
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 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
 260 265 270
 Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
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 Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
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 Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
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 Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
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 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
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 Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr
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 Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro
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 Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu
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 Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe
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 Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu
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 Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp
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 Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly
 530 535 540
 Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu
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 Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp
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 Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys
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Pro	His	Leu 35	Pro	Arg	Pro	His	Ser 40	Arg	Val	Pro	Pro	His 45	Pro	Ser	Ser
Glu	Arg 50	Arg	Ala	Val	Tyr	Ile 55	Gly	Ala	Leu	Phe	Pro 60	Met	Ser	Gly	Gly
Trp 65	Pro	Gly	Gly	Gln	Ala 70	Cys	Gln	Pro	Ala	Val 75	Glu	Met	Ala	Leu	Glu 80
Asp	Val	Asn	Ser	Arg 85	Arg	Asp	Ile	Leu	Pro 90	Asp	Tyr	Glu	Leu	Lys 95	Leu
Ile	His	His	Asp 100	Ser	Lys	Cys	Asp	Pro 105	Gly	Gln	Ala	Thr	Lys 110	Tyr	Leu
Tyr	Glu	Leu 115	Leu	Tyr	Asn	Asp	Pro 120	Ile	Lys	Ile	Ile	Leu 125	Met	Pro	Gly
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Gln	Arg	Phe	Pro	Thr 165	Phe	Phe	Arg	Thr	His 170	Pro	Ser	Ala	Thr	Leu 175	His
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Ala	Thr	Ile 195	Gln	Gln	Thr	Thr	Glu 200	Val	Phe	Thr	Ser	Thr 205	Leu	Asp	Asp
Leu	Glu 210	Glu	Arg	Val	Lys	Glu 215	Ala	Gly	Ile	Glu	Ile 220	Thr	Phe	Arg	Gln
Ser 225	Phe	Phe	Ser	Asp	Pro 230	Ala	Val	Pro	Val	Lys 235	Asn	Leu	Lys	Arg	Gln 240
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 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
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 Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
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 Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
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 Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
 405 410 415
 Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
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 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile
 450 455 460
 Lys Thr Phe Arg Phe Leu Ser Gln Lys
 465 470

<210> 4
 <211> 480
 <212> PRT
 <213> Human

<400> 4

Met Ala Ser Pro Arg Ser Ser Gly Gln Pro Gly Pro Xaa Pro Pro Pro
 1 5 10 15
 Pro Pro Pro Pro Ala Arg Leu Leu Leu Leu Leu Leu Leu Pro Leu Leu
 20 25 30
 Leu Pro Leu Ala Pro Gly Ala Trp Gly Trp Ala Arg Gly Ala Pro Arg

35					40					45					
Pro	Pro	Pro	Ser	Ser	Pro	Pro	Leu	Ser	Ile	Met	Gly	Leu	Met	Pro	Leu
50					55					60					
Thr	Lys	Glu	Val	Ala	Lys	Gly	Ser	Ile	Gly	Arg	Gly	Val	Leu	Pro	Ala
65					70					75					80
Val	Glu	Leu	Ala	Ile	Glu	Gln	Ile	Arg	Asn	Glu	Ser	Leu	Leu	Arg	Pro
				85					90					95	
Tyr	Phe	Leu	Asp	Leu	Arg	Leu	Tyr	Asp	Thr	Glu	Cys	Asp	Asn	Ala	Lys
			100					105					110		
Gly	Leu	Lys	Ala	Phe	Tyr	Asp	Ala	Ile	Lys	Tyr	Gly	Pro	Asn	His	Leu
		115					120					125			
Met	Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr	Ser	Ile	Ile	Ala	Glu
	130					135					140				
Ser	Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Thr
145					150					155					160
Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Phe	Phe	Arg	Thr	Val
				165					170					175	
Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu	Lys	Leu	Leu	Lys	His
			180					185					190		
Tyr	Gln	Trp	Lys	Arg	Val	Gly	Thr	Leu	Thr	Gln	Asp	Val	Gln	Arg	Phe
		195					200					205			
Ser	Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu	Tyr	Gly	Glu	Asp	Ile
	210					215					220				
Glu	Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp	Pro	Cys	Thr	Ser	Val
225					230					235					240
Lys	Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile	Leu	Gly	Gln	Phe	Asp
				245					250					255	
Gln	Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala	Tyr	Glu	Glu	Asn	Met
			260					265					270		
Tyr	Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly	Trp	Tyr	Glu	Pro	Ser
		275					280					285			
Trp	Trp	Glu	Gln	Val	His	Thr	Glu	Ala	Asn	Ser	Ser	Arg	Cys	Leu	Arg
	290					295					300				
Lys	Asn	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile	Gly	Val	Asp	Phe	Glu
305					310					315					320
Pro	Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser	Gly	Lys	Thr	Pro	Gln
				325					330					335	

Gln Tyr Glu Arg Glu Tyr Asn Asn Lys Arg Ser Gly Val Gly Pro Ser
 340 345 350
 Lys Phe His Gly Tyr Ala Tyr Asp Gly Ile Trp Val Ile Ala Lys Thr
 355 360 365
 Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg
 370 375 380
 Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu
 385 390 395 400
 Asn Ala Met Asn Glu Thr Asn Phe Phe Gly Val Thr Gly Gln Val Val
 405 410 415
 Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln
 420 425 430
 Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr
 435 440 445
 Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln Gly Ser Glu Pro Pro
 450 455 460
 Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg Lys Ile Ser Leu Pro
 465 470 475 480

<210> 5
 <211> 583
 <212> PRT
 <213> Human

<400> 5

Met Val Cys Glu Gly Lys Arg Ser Ala Ser Cys Pro Cys Phe Phe Leu
 1 5 10 15
 Leu Thr Ala Lys Phe Tyr Trp Ile Leu Thr Met Met Gln Arg Thr His
 20 25 30
 Ser Gln Glu Tyr Ala His Ser Ile Arg Val Asp Gly Asp Ile Ile Leu
 35 40 45
 Gly Gly Leu Phe Pro Val His Ala Lys Gly Glu Arg Gly Val Pro Cys
 50 55 60
 Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
 65 70 75 80
 Tyr Ala Ile Asp Gln Ile Asn Lys Asp Pro Asp Leu Leu Ser Asn Ile
 85 90 95
 Thr Leu Gly Val Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala
 100 105 110

Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu Lys Asp Ala
 115 120 125
 Ser Asp Val Lys Cys Ala Asn Gly Asp Pro Pro Ile Phe Thr Lys Pro
 130 135 140
 Asp Lys Ile Ser Gly Val Ile Gly Ala Ala Ala Ser Ser Val Ser Ile
 145 150 155 160
 Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
 165 170 175
 Ala Ser Thr Ala Pro Glu Leu Ser Asp Asn Thr Arg Tyr Asp Phe Phe
 180 185 190
 Ser Arg Val Val Pro Pro Asp Ser Tyr Gln Ala Gln Ala Met Val Asp
 195 200 205
 Ile Val Thr Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu
 210 215 220
 Gly Asn Tyr Gly Glu Ser Gly Val Glu Ala Phe Thr Gln Ile Ser Arg
 225 230 235 240
 Glu Ile Gly Gly Val Cys Ile Ala Gln Ser Gln Lys Ile Pro Arg Glu
 245 250 255
 Pro Arg Pro Gly Glu Phe Glu Lys Ile Ile Lys Arg Leu Leu Glu Thr
 260 265 270
 Pro Asn Ala Arg Ala Val Ile Met Phe Ala Asn Glu Asp Asp Ile Arg
 275 280 285
 Arg Ile Leu Glu Ala Ala Lys Lys Leu Asn Gln Ser Gly His Phe Leu
 290 295 300
 Trp Ile Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Tyr Gln
 305 310 315 320
 Gln Glu Glu Ile Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Ala
 325 330 335
 Ser Ile Asp Gly Phe Asp Arg Tyr Phe Arg Ser Arg Thr Leu Ala Asn
 340 345 350
 Asn Arg Arg Asn Val Trp Phe Ala Glu Phe Trp Glu Glu Asn Phe Gly
 355 360 365
 Cys Lys Leu Gly Ser His Gly Lys Arg Asn Ser His Ile Lys Lys Cys
 370 375 380
 Thr Gly Leu Glu Arg Ile Ala Arg Asp Ser Ser Tyr Glu Gln Glu Gly
 385 390 395 400
 Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ser Met Ala Tyr Ala Leu
 405 410 415

His Asn Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro
 420 425 430
 Arg Met Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala
 435 440 445
 Val Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Thr Phe Asn Glu Asn
 450 455 460
 Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Ile Thr Asn
 465 470 475 480
 Lys Ser Thr Glu Tyr Lys Val Ile Gly His Trp Thr Asn Gln Leu His
 485 490 495
 Leu Lys Val Glu Asp Met Gln Trp Ala His Arg Glu His Thr His Pro
 500 505 510
 Ala Ser Val Cys Ser Leu Pro Cys Lys Pro Gly Glu Arg Lys Lys Thr
 515 520 525
 Val Lys Gly Val Pro Cys Cys Trp His Cys Glu Arg Cys Glu Gly Tyr
 530 535 540
 Asn Tyr Gln Val Asp Glu Leu Ser Cys Glu Leu Cys Pro Leu Asp Gln
 545 550 555 560
 Arg Pro Asn Met Asn Arg Thr Gly Cys Gln Leu Ile Pro Ile Ile Lys
 565 570 575
 Leu Glu Trp His Ser Pro Trp
 580

<210> 6
 <211> 250
 <212> PRT
 <213> Human

<400> 6

Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile Phe Leu Thr Ala
 1 5 10 15
 Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys
 20 25 30
 Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Leu Cys
 35 40 45
 Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro Gln Asp Trp Thr
 50 55 60
 Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile

65		70		75		80
Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala						
		85		90		95
Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly Leu Asn Leu Gln						
		100		105		110
Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile Val Ile Cys Val						
		115		120		125
Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn Gln Glu Leu						
		130		135		140
Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly Ser Leu Met Ala						
		145		150		155
Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe						
		165		170		175
Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala						
		180		185		190
Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser						
		195		200		205
Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val						
		210		215		220
Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile						
		225		230		235
Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe						
		245		250		

<210> 7
 <211> 267
 <212> PRT
 <213> Human

<400> 7

Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala						
1			5		10	15
Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile						
		20		25		30
Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser						
		35		40		45
Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile						
		50		55		60

Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
 65 70 75 80
 Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
 85 90 95
 Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
 100 105 110
 Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
 115 120 125
 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
 130 135 140
 His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
 145 150 155 160
 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
 165 170 175
 Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
 180 185 190
 Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 195 200 205
 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 210 215 220
 Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 225 230 235 240
 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 245 250 255
 Ile Thr Leu Val Val Leu Phe Val Pro Lys Met
 260 265

<210> 8
 <211> 267
 <212> PRT
 <213> Human

<400> 8

Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala
 1 5 10 15
 Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
 20 25 30
 Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
 35 40 45

Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile
 50 55 60
 Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
 65 70 75 80
 Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
 85 90 95
 Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
 100 105 110
 Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
 115 120 125
 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
 130 135 140
 His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
 145 150 155 160
 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
 165 170 175
 Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
 180 185 190
 Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 195 200 205
 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 210 215 220
 Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 225 230 235 240
 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 245 250 255
 Ile Thr Leu Val Val Leu Phe Val Pro Lys Met
 260 265

<210> 9
 <211> 264
 <212> PRT
 <213> Human

<400> 9

Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala
 1 5 10 15

Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
 20 25 30
 Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
 35 40 45
 Leu Ser Tyr Ala Ser Ile Phe Leu Phe Gly Leu Asp Gly Ser Phe Val
 50 55 60
 Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val Arg Thr Trp Ile Leu
 65 70 75 80
 Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met Phe Ala Lys Thr Trp
 85 90 95
 Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Lys Ile Ile
 100 105 110
 Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
 115 120 125
 Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr
 130 135 140
 Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
 145 150 155 160
 Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp
 165 170 175
 Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys
 180 185 190
 Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile Pro Ala Leu Asn Asp
 195 200 205
 Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val Gly Ile Met Cys Ile
 210 215 220
 Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp Gln Pro Asn Val Gln
 225 230 235 240
 Phe Cys Ile Val Ala Leu Val Ile Ile Phe Cys Ser Thr Ile Thr Leu
 245 250 255
 Cys Leu Val Phe Val Pro Lys Leu
 260

<210>	10
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<212>	PRT
<213>	Human

<400> 10

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<210> 11
 <211> 216
 <212> PRT
 <213> Human

<400> 11

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Lys Pro Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala
 1          5          10          15

His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val
      20          25          30

Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro
      35          40          45

Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln
 50          55          60

Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu
65          70          75          80

Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln
      85          90          95

Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr
      100          105          110

Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly
      115          120          125

Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr
      130          135          140

Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp
145          150          155          160

Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly
      165          170          175

Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu
      180          185          190

Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr
      195          200          205

Val Thr Glu Asn Val Val Asn Ser
      210          215

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<210> 12
 <211> 104
 <212> PRT
 <213> Human

<400> 12

Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr
 1 5 10 15
 Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg
 20 25 30
 Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys
 35 40 45
 Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln
 50 55 60
 Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly
 65 70 75 80
 Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly
 85 90 95
 Ser Arg Val His Leu Leu Tyr Lys
 100

<210> 13
 <211> 104
 <212> PRT
 <213> Human

<400> 13

Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr
 1 5 10 15
 Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg
 20 25 30
 Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys
 35 40 45
 Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln
 50 55 60
 Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly
 65 70 75 80
 Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly
 85 90 95
 Ser Arg Val His Leu Leu Tyr Lys
 100

<400> 14

[illegible]

<210> 15
 <211> 65
 <212> PRT
 <213> Human

<400> 15

His	Pro	Glu	Gln	Asn	Val	Gln	Lys	Arg	Lys	Arg	Ser	Phe	Lys	Ala	Val
1				5					10					15	
Val	Thr	Ala	Ala	Thr	Met	Gln	Ser	Lys	Leu	Ile	Gln	Lys	Gly	Asn	Asp
			20					25					30		
Arg	Pro	Asn	Gly	Glu	Val	Lys	Ser	Glu	Leu	Cys	Glu	Ser	Leu	Glu	Thr
		35					40					45			
Asn	Ser	Lys	Ser	Ser	Val	Glu	Phe	Pro	Met	Val	Lys	Ser	Gly	Ser	Thr
	50					55					60				

Ser
 65

<210> 16
 <211> 374
 <212> PRT
 <213> Human

<400> 16

Met	Ala	Arg	Ser	Leu	Thr	Trp	Gly	Cys	Cys	Pro	Trp	Cys	Leu	Thr	Glu
1				5					10					15	
Glu	Glu	Lys	Thr	Ala	Ala	Arg	Ile	Asp	Gln	Glu	Ile	Asn	Arg	Ile	Leu
			20					25					30		
Leu	Glu	Gln	Lys	Lys	Gln	Glu	Arg	Glu	Glu	Leu	Lys	Leu	Leu	Leu	Leu
		35					40					45			
Gly	Pro	Gly	Glu	Ser	Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln	Met	Arg	Ile
	50					55					60				
Ile	His	Gly	Val	Gly	Tyr	Ser	Glu	Glu	Asp	Arg	Arg	Ala	Phe	Arg	Leu
65					70				75						80
Leu	Ile	Tyr	Gln	Asn	Ile	Phe	Val	Ser	Met	Gln	Ala	Met	Ile	Asp	Ala
				85					90					95	
Met	Asp	Arg	Leu	Gln	Ile	Pro	Phe	Ser	Arg	Pro	Asp	Ser	Lys	Gln	His
			100					105					110		
Ala	Ser	Leu	Val	Met	Thr	Gln	Asp	Pro	Tyr	Lys	Val	Ser	Thr	Phe	Glu
		115					120					125			
Lys	Pro	Tyr	Ala	Val	Ala	Met	Gln	Tyr	Leu	Trp	Arg	Asp	Ala	Gly	Ile
	130					135					140				

Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
 145 150 155 160
 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile
 165 170 175
 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
 180 185 190
 Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp
 195 200 205
 Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu
 210 215 220
 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
 225 230 235 240
 Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala
 245 250 255
 Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
 260 265 270
 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr
 275 280 285
 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp
 290 295 300
 Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr
 305 310 315 320
 Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala
 325 330 335
 Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val
 340 345 350
 Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
 355 360 365
 Asp Glu Ile Asn Leu Leu
 370

<400> 17

Met 1	Ala	Arg	Ser	Leu 5	Thr	Trp	Arg	Cys	Cys 10	Pro	Trp	Cys	Leu	Thr 15	Glu
Asp	Glu	Lys	Ala 20	Ala	Ala	Arg	Val	Asp 25	Gln	Glu	Ile	Asn	Arg 30	Ile	Leu
Leu	Glu	Gln 35	Lys	Lys	Gln	Asp	Arg 40	Gly	Glu	Leu	Lys	Leu 45	Leu	Leu	Leu
Gly 50	Pro	Gly	Glu	Ser	Gly	Lys 55	Ser	Thr	Phe	Ile	Lys 60	Gln	Met	Arg	Ile
Ile 65	His	Gly	Ala	Gly	Tyr 70	Ser	Glu	Glu	Glu	Arg 75	Lys	Gly	Phe	Arg	Pro 80
Leu	Val	Tyr	Gln	Asn 85	Ile	Phe	Val	Ser	Met 90	Arg	Ala	Met	Ile	Glu 95	Ala
Met	Glu	Arg	Leu 100	Gln	Ile	Pro	Phe	Ser 105	Arg	Pro	Glu	Ser	Lys 110	His	His
Ala	Ser	Leu 115	Val	Met	Ser	Gln	Asp 120	Pro	Tyr	Lys	Val	Thr 125	Thr	Phe	Glu
Lys 130	Arg	Tyr	Ala	Ala	Ala	Met 135	Gln	Trp	Leu	Trp	Arg 140	Asp	Ala	Gly	Ile
Arg 145	Ala	Cys	Tyr	Glu	Arg 150	Arg	Arg	Glu	Phe	His 155	Leu	Leu	Asp	Ser	Ala 160
Val	Tyr	Tyr	Leu	Ser 165	His	Leu	Glu	Arg	Ile 170	Thr	Glu	Glu	Gly	Tyr 175	Val
Pro	Thr	Ala	Gln 180	Asp	Val	Leu	Arg	Ser 185	Arg	Met	Pro	Thr	Thr 190	Gly	Ile
Asn	Glu	Tyr 195	Cys	Phe	Ser	Val	Gln 200	Lys	Thr	Asn	Leu	Arg 205	Ile	Val	Asp
Val 210	Gly	Gly	Gln	Lys	Ser	Glu 215	Arg	Lys	Lys	Trp	Ile 220	His	Cys	Phe	Glu
Asn 225	Val	Ile	Ala	Leu	Ile 230	Tyr	Leu	Ala	Ser 235	Leu	Ser	Glu	Tyr	Asp	Gln 240
Cys	Leu	Glu	Glu	Asn 245	Asn	Gln	Glu	Asn	Arg 250	Met	Lys	Glu	Ser	Leu 255	Ala
Leu	Phe	Gly	Thr 260	Ile	Leu	Glu	Leu	Pro 265	Trp	Phe	Lys	Ser	Thr 270	Ser	Val

Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
 275 280 285
 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
 290 295 300
 Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
 305 310 315 320
 Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser
 325 330 335
 Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
 340 345 350
 Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
 355 360 365
 Asp Glu Ile Asn Leu Leu
 370

<210> 18
 <211> 3234
 <212> DNA
 <213> Human

<400> 18

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gggccagacc	agcgagccca	aaagaagggg	gacattatcc	ttgggggggt	ctttcctatt	120
catttttgag	tagcagctaa	agatcaagat	ctcaaataca	ggccggagtc	tgtggaatgt	180
atcaggtata	atttccgtgg	gtttcgctgg	ttacaggcta	tgatatttgc	catagaggag	240
ataaacagca	gcccagccct	tcttcccaac	ttgacgctgg	gatacaggat	atttgacact	300
tgcaacaccg	tttctaaggc	cttgggaagcc	accctgagtt	ttgttgctca	aaacaaaatt	360
gattctttga	accttgatga	gttctgcaac	tgctcagagc	acattccctc	tacgattgct	420
gtggtgggag	caactggctc	aggcgtctcc	acggcagtg	caaactctgt	ggggctcttc	480
tacattcccc	aggtcagtta	tgccctcctc	agcagactcc	tcagcaacaa	gaatcaattc	540
aagtctttcc	tccgaaccat	ccccaatgat	gagcaccagg	ccactgccat	ggcagacatc	600
atcgagtatt	tccgctggaa	ctgggtgggc	acaattgcag	ctgatgacga	ctatgggcgg	660
ccggggattg	agaaattccg	agaggaagct	gaggaaaggg	atatctgcat	cgacttcagt	720
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<400> 22

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Gln	Val 50	Lys	Ala	Ile	Asn	Phe 55	Leu	Pro	Val	Asp	Tyr 60	Glu	Ile	Glu	Tyr
Val 65	Cys	Arg	Gly	Glu	Arg 70	Glu	Val	Val	Gly	Pro 75	Lys	Val	Arg	Lys 80	Cys
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Arg	Ile	Cys	Ser 100	Lys	Ser	Tyr	Leu	Thr 105	Leu	Glu	Asn	Gly	Lys 110	Val	Phe
Leu	Thr	Gly 115	Gly	Asp	Leu	Pro	Ala 120	Leu	Asp	Gly	Ala	Arg 125	Val	Glu	Phe
Arg	Cys 130	Asp	Pro	Asp	Phe	His 135	Leu	Val	Gly	Ser	Ser 140	Arg	Ser	Val	Cys
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Glu 210	Leu	Lys	Leu	Ile	His	His 215	Asp	Ser	Lys	Cys	Asp 220	Pro	Gly	Gln	Ala
Thr 225	Lys	Tyr	Leu	Tyr	Glu 230	Leu	Leu	Tyr	Asn	Asp 235	Pro	Ile	Lys	Ile 240	Ile
Leu	Met	Pro	Gly	Cys 245	Ser	Ser	Val	Ser	Thr 250	Leu	Val	Ala	Glu	Ala 255	Ala
Arg	Met	Trp	Asn 260	Leu	Ile	Val	Leu	Ser 265	Tyr	Gly	Ser	Ser	Ser 270	Pro	Ala

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 290 295 300
 Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser
 305 310 315 320
 Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile
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 Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn
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 Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly
 370 375 380
 Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe
 385 390 395 400
 Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu
 405 410 415
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Ile Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile
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 Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp
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 Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr
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 740 745 750
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 755 760 765
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 Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp
 785 790 795 800
 His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu
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 Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu
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 Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu
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 Trp Gln Ser Glu Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn

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Thr	Pro	Pro	Asp	Pro	Ser	Gly	Gly	Leu	Pro	Arg	Gly	Pro	Ser	Glu	Pro
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<400> 25

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Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	Ala	Arg	Met	Trp	Asn
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Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His

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Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg
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Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg
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 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu
 740 745 750
 Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu

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Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg	Glu Leu Glu Lys Ile	
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Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln		
785	790	795 800
Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp		
805	810	815
Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu		
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Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys		
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<210> 26
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 <212> DNA
 <213> Human

<400> 26

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<210> 27
 <211> 824
 <212> PRT
 <213> Human

<400> 27

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Val Leu Gly Gly Leu Phe Pro Val His Gln Lys Gly Gly Pro Ala Glu
      35           40           45

Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala
      50           55           60

Met Leu Phe Ala Leu Asp Arg Ile Asn Arg Asp Pro His Leu Leu Pro
      65           70           75           80

Gly Val Arg Leu Gly Ala His Ile Leu Asp Ser Cys Ser Lys Asp Thr
      85           90           95

His Ala Leu Glu Gln Ala Leu Asp Phe Val Arg Ala Ser Leu Ser Arg
      100          105          110

Gly Ala Asp Gly Ser Arg His Ile Cys Pro Asp Gly Ser Tyr Ala Thr
      115          120          125

His Gly Asp Ala Pro Thr Ala Ile Thr Gly Val Ile Gly Gly Ser Tyr
      130          135          140

Ser Asp Val Ser Ile Gln Val Ala Asn Leu Leu Arg Leu Phe Gln Ile
      145          150          155          160

Pro Gln Ile Ser Tyr Ala Ser Thr Ser Ala Lys Leu Ser Asp Lys Ser
      165          170          175

Arg Tyr Asp Tyr Phe Ala Arg Thr Val Pro Pro Asp Phe Phe Gln Ala

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Thr	Ala	Phe	Ser	Val	Cys	Tyr	Ser	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg
				645					650					655	
Ile	Ala	Arg	Ile	Phe	Gly	Gly	Ala	Arg	Glu	Gly	Ala	Gln	Arg	Pro	Arg
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Phe	Ile	Ser	Pro	Ala	Ser	Gln	Val	Ala	Ile	Cys	Leu	Ala	Leu	Ile	Ser
		675					680					685			
Gly	Gln	Leu	Leu	Ile	Val	Val	Ala	Trp	Leu	Val	Val	Glu	Ala	Pro	Gly
	690					695					700				
Thr	Gly	Lys	Glu	Thr	Ala	Pro	Glu	Arg	Arg	Glu	Val	Val	Thr	Leu	Arg
705					710					715					720
Cys	Asn	His	Arg	Asp	Ala	Ser	Met	Leu	Gly	Ser	Leu	Ala	Tyr	Asn	Val
				725					730					735	
Leu	Leu	Ile	Ala	Leu	Cys	Thr	Leu	Tyr	Ala	Phe	Asn	Thr	Arg	Lys	Cys
			740						745				750		
Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	Phe	Ile	Gly	Phe	Thr	Met	Tyr	Thr
		755					760					765			
Thr	Cys	Ile	Ile	Trp	Leu	Ala	Leu	Leu	Pro	Ile	Phe	Tyr	Val	Thr	Ser
						775						780			

Ser Asp Tyr Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu
785 790 795 800

Ser Gly Ser Val Val Leu Gly Cys Leu Phe Ala Pro Lys Leu His Ile
805 810 815

Ile Leu Phe Gln Pro Gln Lys Asn
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<210> 28

<211> 1077

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Gqi5

<400> 28

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<210> 29

<211> 359

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Gqi5

<400> 29

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20 25 30

Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly

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Ser	Gly	Tyr	Ser	Asp	Glu	Asp	Lys	Arg	Gly	Phe	Thr	Lys	Leu	Val	Tyr
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Gln	Asn	Ile	Phe	Thr	Ala	Met	Gln	Ala	Met	Ile	Arg	Ala	Met	Asp	Thr
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Leu	Lys	Ile	Pro	Tyr	Lys	Tyr	Glu	His	Asn	Lys	Ala	His	Ala	Gln	Leu
			100					105						110	
Val	Arg	Glu	Val	Asp	Val	Glu	Lys	Val	Ser	Ala	Phe	Glu	Asn	Pro	Tyr
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Val	Asp	Ala	Ile	Lys	Ser	Leu	Trp	Asn	Asp	Pro	Gly	Ile	Gln	Glu	Cys
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Tyr	Asp	Arg	Arg	Arg	Glu	Tyr	Gln	Leu	Ser	Asp	Ser	Thr	Lys	Tyr	Tyr
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Leu	Asn	Asp	Leu	Asp	Arg	Val	Ala	Asp	Pro	Ala	Tyr	Leu	Pro	Thr	Gln
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Gln	Asp	Val	Leu	Arg	Val	Arg	Val	Pro	Thr	Thr	Gly	Ile	Ile	Glu	Tyr
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Pro	Phe	Asp	Leu	Gln	Ser	Val	Ile	Phe	Arg	Met	Val	Asp	Val	Gly	Gly
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Glu	Ser	Asp	Asn	Glu	Asn	Arg	Met	Glu	Glu	Ser	Lys	Ala	Leu	Phe	Arg
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			260					265					270		
Leu	Asn	Lys	Lys	Asp	Leu	Leu	Glu	Glu	Lys	Ile	Met	Tyr	Ser	His	Leu
		275					280					285			
Val	Asp	Tyr	Phe	Pro	Glu	Tyr	Asp	Gly	Pro	Gln	Arg	Asp	Ala	Gln	Ala
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Ala	Arg	Glu	Phe	Ile	Leu	Lys	Met	Phe	Val	Asp	Leu	Asn	Pro	Asp	Ser
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Asp	Lys	Ile	Ile	Tyr	Ser	His	Phe	Thr	Cys	Ala	Thr	Asp	Thr	Glu	Asn
				325					330					335	
Ile	Arg	Phe	Val	Phe	Ala	Ala	Val	Lys	Asp	Thr	Ile	Leu	Gln	Leu	Asn

340

345

350

Leu Lys Asp Cys Gly Leu Phe
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<210> 30

<211> 2751

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric hCAR/hmGluR2

<400> 30

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<210> 31
<211> 917
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric hCAR/hmGluR2

<400> 31

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      20          25          30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
      35          40          45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
      50          55          60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
      65          70          75          80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
      85          90          95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
      100          105          110

Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
      115          120          125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
      130          135          140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
      145          150          155          160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
      165          170          175

Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
      180          185          190

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
      195          200          205

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Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
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 Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
 225 230 235 240
 Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
 245 250 255
 Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
 260 265 270
 Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
 275 280 285
 Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
 290 295 300
 Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
 305 310 315 320
 Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
 325 330 335
 Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
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 Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
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 Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
 370 375 380
 Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
 385 390 395 400
 Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
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 Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
 420 425 430
 Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
 435 440 445
 Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
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 Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
 465 470 475 480
 Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
 485 490 495

Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
 500 505 510
 Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
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 Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
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 <400> 32

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 <400> 33

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<223> Chimeric hmGluR2/hCaR

<400> 35

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Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala

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Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro
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Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser
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 <211> 4185
 <212> DNA
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<220>
 <223> Chimeric pmGluR2//CaR*G(qi5)

<400> 36

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<211> 1394

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric pmGluR2//CaR*G(qi5)

<400> 37

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Met	Leu	Phe	Ala	Leu	Asp	Arg	Ile	Asn	Arg	Asp	Pro	His	Leu	Leu	Pro	65	70	75	80
Gly	Val	Arg	Leu	Gly	Ala	His	Ile	Leu	Asp	Ser	Cys	Ser	Lys	Asp	Thr	85	90	95	
His	Ala	Leu	Glu	Gln	Ala	Leu	Asp	Phe	Val	Arg	Ala	Ser	Leu	Ser	Arg	100	105	110	
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Ser	Asp	Val	Ser	Ile	Gln	Val	Ala	Asn	Leu	Leu	Arg	Leu	Phe	Gln	Ile	145	150	155	160
Pro	Gln	Ile	Ser	Tyr	Ala	Ser	Thr	Ser	Ala	Lys	Leu	Ser	Asp	Lys	Ser	165	170	175	
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Lys	Ala	Met	Ala	Glu	Ile	Leu	Arg	Phe	Phe	Asn	Trp	Thr	Tyr	Val	Ser	195	200	205	
Thr	Val	Ala	Ser	Glu	Gly	Asp	Tyr	Gly	Glu	Thr	Gly	Ile	Glu	Ala	Phe	210	215	220	
Glu	Leu	Glu	Ala	Arg	Ala	Arg	Asn	Ile	Cys	Val	Ala	Thr	Ser	Glu	Lys	225	230	235	240
Val	Gly	Arg	Ala	Met	Ser	Arg	Ala	Ala	Phe	Glu	Gly	Val	Val	Arg	Ala	245	250	255	
Leu	Leu	Gln	Lys	Pro	Ser	Ala	Arg	Val	Ala	Val	Leu	Phe	Thr	Arg	Ser	260	265	270	
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Gln	Pro	Gly	Glu	Val	Cys	Cys	Trp	Leu	Cys	Ile	Pro	Cys	Gln	Pro	Tyr			
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Thr	Ala	Phe	Ser	Val	Cys	Tyr	Ser	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg			
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Phe	Ile	Ser	Pro	Ala	Ser	Gln	Val	Ala	Ile	Cys	Leu	Ala	Leu	Ile	Ser			
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Thr	Gly	Lys	Glu	Thr	Ala	Pro	Glu	Arg	Arg	Glu	Val	Val	Thr	Leu	Arg			
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Cys	Asn	His	Arg	Asp	Ala	Ser	Met	Leu	Gly	Ser	Leu	Ala	Tyr	Asn	Val			
				725					730					735				
Leu	Leu	Ile	Ala	Leu	Cys	Thr	Leu	Tyr	Ala	Phe	Lys	Thr	Arg	Lys	Cys			
			740					745					750					
Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	Phe	Ile	Gly	Phe	Thr	Met	Tyr	Thr			
		755					760					765						
Thr	Cys	Ile	Ile	Trp	Leu	Ala	Phe	Leu	Pro	Ile	Phe	Tyr	Val	Thr	Ser			
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Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser	Ser	Lys	Ser	Asn	Ser	Glu	Asp	Pro			
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Phe	Pro	Gln	Pro	Glu	Arg	Gln	Lys	Gln	Gln	Gln	Pro	Leu	Ala	Leu	Thr			

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885								890				895			
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Val	Gly	Gly	Asp	Gln	Arg	Pro	Glu	Val	Glu	Asp	Pro	Glu	Glu	Leu	Ser
			995					1000					1005		
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Glu	Asp	Lys	Arg	Gly	Phe	Thr	Lys	Leu	Val	Tyr	Gln	Asn	Ile	Phe	Thr
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Glu Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp
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 Arg Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg
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 Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe
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<213> Artificial Sequence

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<223> Chimeric hmGluR8/hCaR

<400> 38

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120

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<220>
 <223> Chimeric hmGluR8/hCaR

<400> 39

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Leu	Thr	Ala	Lys	Phe	Tyr	Trp	Ile	Leu	Thr	Met	Met	Gln	Arg	Thr	His
			20					25					30		
Ser	Gln	Glu	Tyr	Ala	His	Ser	Ile	Arg	Val	Asp	Gly	Asp	Ile	Ile	Leu
		35					40					45			
Gly	Gly	Leu	Phe	Pro	Val	His	Ala	Lys	Gly	Glu	Arg	Gly	Val	Pro	Cys
		50				55					60				
Gly	Glu	Leu	Lys	Lys	Glu	Lys	Gly	Ile	His	Arg	Leu	Glu	Ala	Met	Leu
65					70					75					80
Tyr	Ala	Ile	Asp	Gln	Ile	Asn	Lys	Asp	Pro	Asp	Leu	Leu	Ser	Asn	Ile
				85					90					95	
Thr	Leu	Gly	Val	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala
			100					105					110		
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp	Ala
			115					120				125			
Ser	Asp	Val	Lys	Cys	Ala	Asn	Gly	Asp	Pro	Pro	Ile	Phe	Thr	Lys	Pro
	130					135					140				
Asp	Lys	Ile	Ser	Gly	Val	Ile	Gly	Ala	Ala	Ala	Ser	Ser	Val	Ser	Ile
145					150				155						160
Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr
			165						170					175	
Ala	Ser	Thr	Ala	Pro	Glu	Leu	Ser	Asp	Asn	Thr	Arg	Tyr	Asp	Phe	Phe
			180					185					190		
Ser	Arg	Val	Val	Pro	Pro	Asp	Ser	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp
		195					200					205			
Ile	Val	Thr	Ala	Leu	Gly	Trp	Asn	Tyr	Val	Ser	Thr	Leu	Ala	Ser	Glu
	210					215					220				
Gly	Asn	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Thr	Gln	Ile	Ser	Arg
225					230					235					240
Glu	Ile	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Gln	Lys	Ile	Pro	Arg	Glu
			245						250					255	

Pro	Arg	Pro	Gly	Glu	Phe	Glu	Lys	Ile	Ile	Lys	Arg	Leu	Leu	Glu	Thr	260	265	270
Pro	Asn	Ala	Arg	Ala	Val	Ile	Met	Phe	Ala	Asn	Glu	Asp	Asp	Ile	Arg	275	280	285
Arg	Ile	Leu	Glu	Ala	Ala	Lys	Lys	Leu	Asn	Gln	Ser	Gly	His	Phe	Leu	290	295	300
Trp	Ile	Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Tyr	Gln	305	310	315
Gln	Glu	Glu	Ile	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Ala	325	330	335
Ser	Ile	Asp	Gly	Phe	Asp	Arg	Tyr	Phe	Arg	Ser	Arg	Thr	Leu	Ala	Asn	340	345	350
Asn	Arg	Arg	Asn	Val	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Glu	Asn	Phe	Gly	355	360	365
Cys	Lys	Leu	Gly	Ser	His	Gly	Lys	Arg	Asn	Ser	His	Ile	Lys	Lys	Cys	370	375	380
Thr	Gly	Leu	Glu	Arg	Ile	Ala	Arg	Asp	Ser	Ser	Tyr	Glu	Gln	Glu	Gly	385	390	395
Lys	Val	Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ser	Met	Ala	Tyr	Ala	Leu	405	410	415
His	Asn	Met	His	Lys	Asp	Leu	Cys	Pro	Gly	Tyr	Ile	Gly	Leu	Cys	Pro	420	425	430
Arg	Met	Ser	Thr	Ile	Asp	Gly	Lys	Glu	Leu	Leu	Gly	Tyr	Ile	Arg	Ala	435	440	445
Val	Asn	Phe	Asn	Gly	Ser	Ala	Gly	Thr	Pro	Val	Thr	Phe	Asn	Glu	Asn	450	455	460
Gly	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Phe	Gln	Tyr	Gln	Ile	Thr	Asn	465	470	475
Lys	Ser	Thr	Glu	Tyr	Lys	Val	Ile	Gly	His	Trp	Thr	Asn	Gln	Leu	His	485	490	495
Leu	Lys	Val	Glu	Asp	Met	Gln	Trp	Ala	His	Arg	Glu	His	Thr	His	Pro	500	505	510
Ala	Ser	Val	Cys	Ser	Leu	Pro	Cys	Lys	Pro	Gly	Glu	Arg	Lys	Lys	Thr	515	520	525
Val	Lys	Gly	Val	Pro	Cys	Cys	Trp	His	Cys	Glu	Arg	Cys	Glu	Gly	Tyr	530	535	540
Asn	Tyr	Gln	Val	Asp	Glu	Leu	Ser	Cys	Glu	Leu	Cys	Pro	Leu	Asp	Gln	545	550	555

Arg	Pro	Asn	Met	Asn	Arg	Thr	Gly	Cys	Gln	Leu	Ile	Pro	Ile	Ile	Lys	565	570	575	
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Leu	Gly	Ile	Ile	Ala	Thr	Thr	Phe	Val	Ile	Val	Thr	Phe	Val	Arg	Tyr	595	600	605	
Asn	Asp	Thr	Pro	Ile	Val	Arg	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	Val	610	615	620	
Leu	Leu	Thr	Gly	Ile	Phe	Leu	Cys	Tyr	Ser	Ile	Thr	Phe	Leu	Met	Ile	625	630	635	640
Ala	Ala	Pro	Asp	Thr	Ile	Ile	Cys	Ser	Phe	Arg	Arg	Val	Phe	Leu	Gly	645	650	655	
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Ile	His	Arg	Ile	Phe	Glu	Gln	Gly	Lys	Lys	Ser	Val	Thr	Ala	Pro	Lys	675	680	685	
Phe	Ile	Ser	Pro	Ala	Ser	Gln	Leu	Val	Ile	Thr	Phe	Ser	Leu	Ile	Ser	690	695	700	
Val	Gln	Leu	Leu	Gly	Val	Phe	Val	Trp	Phe	Val	Val	Asp	Pro	Pro	His	705	710	715	720
Ile	Ile	Ile	Asp	Tyr	Gly	Glu	Gln	Arg	Thr	Leu	Asp	Pro	Glu	Lys	Ala	725	730	735	
Arg	Gly	Val	Leu	Lys	Cys	Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	Ser	740	745	750	
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Lys	Thr	Arg	Gly	Val	Pro	Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	Gly	770	775	780	
Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Ile	Trp	Leu	Ala	Phe	Ile	Pro	Ile	785	790	795	800
Phe	Phe	Gly	Thr	Ala	Gln	Ser	Ala	Glu	Lys	Met	Tyr	Ile	Gln	Thr	Thr	805	810	815	
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Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val				

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Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg	Ser	Asn	Val	Ser	Arg	Lys	Arg	Ser
865					870					875					880
Ser	Ser	Leu	Gly	Gly	Ser	Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser
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<223> Chimeric mGluR8//CaR*G(qi5

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<223> Chimeric mGluR8//CaR*G(qi5

<400> 41

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          35              40              45
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          50              55              60
Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65              70              75              80
Tyr Ala Ile Asp Gln Ile Asn Lys Asp Pro Asp Leu Leu Ser Asn Ile
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Thr Leu Gly Val Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala
          100              105              110
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Ser Asp Val Lys Cys Ala Asn Gly Asp Pro Pro Ile Phe Thr Lys Pro
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Asp Lys Ile Ser Gly Val Ile Gly Ala Ala Ala Ser Ser Val Ser Ile
145              150              155              160
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 His Asn Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro
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 Arg Met Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala
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<213> Artificial Sequence

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<210> 43

<211> 1303

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric GABA-BR2*Gqo5

<400> 43

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Leu Pro Leu Ala Pro Gly Ala Trp Gly Trp Ala Arg Gly Ala Pro Arg
      35             40             45

Pro Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu
 50             55             60

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Thr	Lys	Glu	Val	Ala	Lys	Gly	Ser	Ile	Gly	Arg	Gly	Val	Leu	Pro	Ala	
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Tyr	Phe	Leu	Asp	Leu	Arg	Leu	Tyr	Asp	Thr	Glu	Cys	Asp	Asn	Ala	Lys	
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Gly	Leu	Lys	Ala	Phe	Tyr	Asp	Ala	Ile	Lys	Tyr	Gly	Pro	Asn	His	Leu	
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Met	Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr	Ser	Ile	Ile	Ala	Glu	
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Ser	Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Thr	
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Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Phe	Phe	Arg	Thr	Val	
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Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu	Lys	Leu	Leu	Lys	His	
			180					185					190			
Tyr	Gln	Trp	Lys	Arg	Val	Gly	Thr	Leu	Thr	Gln	Asp	Val	Gln	Arg	Phe	
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Glu	Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp	Pro	Cys	Thr	Ser	Val	
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Lys	Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile	Leu	Gly	Gln	Phe	Asp	
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Gln	Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala	Tyr	Glu	Glu	Asn	Met	
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Tyr	Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly	Trp	Tyr	Glu	Pro	Ser	
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Trp	Trp	Glu	Gln	Val	His	Thr	Glu	Ala	Asn	Ser	Ser	Arg	Cys	Leu	Arg	
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Lys	Asn	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile	Gly	Val	Asp	Phe	Glu	
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Pro	Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser	Gly	Lys	Thr	Pro	Gln	
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Gln	Tyr	Glu	Arg	Glu	Tyr	Asn	Asn	Lys	Arg	Ser	Gly	Val	Gly	Pro	Ser	
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Lys	Phe	His	Gly	Tyr	Ala	Tyr	Asp	Gly	Ile	Trp	Val	Ile	Ala	Lys	Thr	
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Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg
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 Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu
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 405 410 415
 Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln
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 Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr
 435 440 445
 Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln Gly Ser Glu Pro Pro
 450 455 460
 Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg Lys Ile Ser Leu Pro
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 485 490 495
 Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
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 Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
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 545 550 555 560
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 580 585 590
 Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
 595 600 605
 Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr
 610 615 620
 Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
 625 630 635 640
 Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp
 645 650 655
 Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys

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Phe	Leu	Ala	Trp	Glu	Thr	Arg	Asn	Val	Ser	Ile	Pro	Ala	Leu	Asn	Asp
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Ser	Lys	Tyr	Ile	Gly	Met	Ser	Val	Tyr	Asn	Val	Gly	Ile	Met	Cys	Ile
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Ile	Gly	Ala	Ala	Val	Ser	Phe	Leu	Thr	Arg	Asp	Gln	Pro	Asn	Val	Gln
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Phe	Cys	Ile	Val	Ala	Leu	Val	Ile	Ile	Phe	Cys	Ser	Thr	Ile	Thr	Leu
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Cys	Leu	Val	Phe	Val	Pro	Lys	Leu	Ile	Thr	Leu	Arg	Thr	Asn	Pro	Asp
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Ala	Ala	Thr	Gln	Asn	Arg	Arg	Phe	Gln	Phe	Thr	Gln	Asn	Gln	Lys	Lys
		755					760					765			
Glu	Asp	Ser	Lys	Thr	Ser	Thr	Ser	Val	Thr	Ser	Val	Asn	Gln	Ala	Ser
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Gln	Asp	Thr	Pro	Glu	Lys	Thr	Thr	Tyr	Ile	Lys	Gln	Asn	His	Tyr	Gln
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Asp	Ile	Asn	Ser	Pro	Glu	His	Ile	Gln	Arg	Arg	Leu	Ser	Leu	Gln	Leu
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Pro	Ile	Leu	His	His	Ala	Tyr	Leu	Pro	Ser	Ile	Gly	Gly	Val	Asp	Ala
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Ser	Cys	Val	Ser	Pro	Cys	Val	Ser	Pro	Thr	Ala	Ser	Pro	Arg	His	Arg
		915					920					925			
His	Val	Pro	Pro	Ser	Phe	Arg	Val	Met	Val	Ser	Gly	Leu	Ala	Ala	Ala
	930					935					940				
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 Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly
 980 985 990
 Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly
 995 1000 1005
 Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr
 1010 1015 1020
 Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr
 1025 1030 1035 1040
 Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala His Ala Gln Leu
 1045 1050 1055
 Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr
 1060 1065 1070
 Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys
 1075 1080 1085
 Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr
 1090 1095 1100
 Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln
 1105 1110 1115 1120
 Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr
 1125 1130 1135
 Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val Asp Val Gly Gly
 1140 1145 1150
 Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr
 1155 1160 1165
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 Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg
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 Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe
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 Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu
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 Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala
 1235 1240 1245
 Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser
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Asp Lys Ile Asn Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn
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<210> 44
<211> 3969
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric GABA-BR1a*Gqo5

<400> 44

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<210> 45

<211> 1323

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric GABA-BR α 1*Gqo5

<400> 45

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 20             25             30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35             40             45

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu

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				85					90					95	
Val	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Thr	Leu	Glu	Asn	Gly	Lys	Val
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Phe	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	Arg	Val	Asp
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Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	Arg	Ser	Ile
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Cys	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	Gln	Val	Asn
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Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp
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Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln
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Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala
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Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu
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Ile	Thr	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys
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Thr	Glu	Ala	Arg	Lys	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe		
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Glu	Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro		
			420					425					430				
Ala	Asn	Thr	Arg	Ser	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu		
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Lys	Leu	Thr	Lys	Arg	Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	Gly	Gly	Phe		
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Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala		
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Leu	Asn	Lys	Thr	Ser	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu		
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Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala		
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Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp		
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Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly		
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Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu		
545					550				555						560		
Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp		
				565					570					575			
Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe		
			580					585					590				
Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val		
		595					600					605					
Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn		
	610				615						620						
Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala		
625					630				635						640		
Leu	Ala	Ala	Val	Phe	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	Gly	Arg		
				645					650					655			

Asn	Gln	Phe	Pro	Phe	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	Gly	Leu			
			660					665					670					
Gly	Phe	Ser	Leu	Gly	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	Trp	Val			
		675					680					685						
His	Thr	Val	Phe	Thr	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	Lys	Thr			
	690					695					700							
Leu	Glu	Pro	Trp	Lys	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	Gly	Met			
705					710					715					720			
Asp	Val	Leu	Thr	Leu	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	His	Arg			
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Thr	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val			
			740					745					750					
Ser	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Arg	Lys	Met	Asn	Thr			
		755					760					765						
Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly			
	770					775					780							
Ile	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn			
785				790						795					800			
Asp	His	Arg	Ala	Val	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys			
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Ala	Phe	Ala	Phe	Ala	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	Ile	Thr			
		835					840					845						
Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	Gly			
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Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr	Met	Lys	Thr	Gly	Ser	Ser	Thr			
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Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	Arg			
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Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	Ser	Glu	Leu			
			900					905					910					
Arg	His	Gln	Leu	Gln	Ser	Arg	Gln	Gln	Leu	Arg	Ser	Arg	Arg	His	Pro			
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Pro	Thr	Pro	Pro	Glu	Pro	Ser	Gly	Gly	Leu	Pro	Arg	Gly	Pro	Pro	Glu			
		930				935					940							
Pro	Pro	Asp	Arg	Leu	Ser	Cys	Asp	Gly	Ser	Arg	Val	His	Leu	Leu	Tyr			

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Lys Ala Ala Ala Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu Ser						
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Glu Glu Ala Lys Glu Ala Arg Arg Ile Asn Asp Glu Ile Glu Arg Gln						
		980		985		990
Leu Arg Arg Asp Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu						
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Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg						
		1010		1015		1020
Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr						
		1025		1030		1035
Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg						
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His Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe						
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Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly						
		1090		1095		1100
Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser						
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Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr						
		1125		1130		1135
Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly						
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Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val						
		1155		1160		1165
Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe						
		1170		1175		1180
Glu Asn Val Thr Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp						
		1185		1190		1195
Gln Val Leu Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys						
		1205		1210		1215
Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser						
		1220		1225		1230
Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met						
		1235		1240		1245

Tyr Ser His Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg
 1250 1255 1260

Asp Ala Gln Ala Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu
 1265 1270 1275 1280

Asn Pro Asp Ser Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr
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Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp Thr Ile
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<210> 46

<211> 4231

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric pmGluR2//CaR*G(qi5+3Ala

<400> 46

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caggcactgg	actttgtgcg	tgcctcactc	agccgtgggt	ctgatggctc	acgccacatc	360
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gccgtcaagg	acaccatcct	ccagttgaac	ctgaaggact	gcgggtctgtt	ctaattgtgc	4200
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<210> 47

<211> 1397

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric pmGluR2//CaR*G(qi5+3Ala

<400> 47

Met Gly Ser Leu Leu Ala Leu Pro Ala Leu Leu Leu Leu Trp Gly Ala

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10

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Val Ala Glu Gly Pro Ala Lys Lys Val Leu Thr Leu Glu Gly Asp Leu
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 Val Leu Gly Gly Leu Phe Pro Val His Gln Lys Gly Gly Pro Ala Glu
 35 40 45
 Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala
 50 55 60
 Met Leu Phe Ala Leu Asp Arg Ile Asn Arg Asp Pro His Leu Leu Pro
 65 70 75 80
 Gly Val Arg Leu Gly Ala His Ile Leu Asp Ser Cys Ser Lys Asp Thr
 85 90 95
 His Ala Leu Glu Gln Ala Leu Asp Phe Val Arg Ala Ser Leu Ser Arg
 100 105 110
 Gly Ala Asp Gly Ser Arg His Ile Cys Pro Asp Gly Ser Tyr Ala Thr
 115 120 125
 His Gly Asp Ala Pro Thr Ala Ile Thr Gly Val Ile Gly Gly Ser Tyr
 130 135 140
 Ser Asp Val Ser Ile Gln Val Ala Asn Leu Leu Arg Leu Phe Gln Ile
 145 150 155 160
 Pro Gln Ile Ser Tyr Ala Ser Thr Ser Ala Lys Leu Ser Asp Lys Ser
 165 170 175
 Arg Tyr Asp Tyr Phe Ala Arg Thr Val Pro Pro Asp Phe Phe Gln Ala
 180 185 190
 Lys Ala Met Ala Glu Ile Leu Arg Phe Phe Asn Trp Thr Tyr Val Ser
 195 200 205
 Thr Val Ala Ser Glu Gly Asp Tyr Gly Glu Thr Gly Ile Glu Ala Phe
 210 215 220
 Glu Leu Glu Ala Arg Ala Arg Asn Ile Cys Val Ala Thr Ser Glu Lys
 225 230 235 240
 Val Gly Arg Ala Met Ser Arg Ala Ala Phe Glu Gly Val Val Arg Ala
 245 250 255
 Leu Leu Gln Lys Pro Ser Ala Arg Val Ala Val Leu Phe Thr Arg Ser
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 Glu Asp Ala Arg Glu Leu Leu Ala Ala Ser Gln Arg Leu Asn Ala Ser
 275 280 285
 Phe Thr Trp Val Ala Ser Asp Gly Trp Gly Ala Leu Glu Ser Val Val
 290 295 300
 Ala Gly Ser Glu Gly Ala Ala Glu Gly Ala Ile Thr Ile Glu Leu Ala

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Ser Tyr Pro Ile	Ser Asp Phe Ala Ser Tyr Phe Gln Ser Leu Asp Pro					
	325		330		335	
Trp Asn Asn Ser Arg Asn Pro Trp Phe Arg Glu Phe Trp Glu Gln Arg						
	340		345		350	
Phe Arg Cys Ser Phe Arg Gln Arg Asp Cys Ala Ala His Ser Leu Arg						
	355		360		365	
Ala Val Pro Phe Glu Gln Glu Ser Lys Ile Met Phe Val Val Asn Ala						
	370		375		380	
Val Tyr Ala Met Ala His Ala Leu His Asn Met His Arg Ala Leu Cys						
385		390		395		400
Pro Asn Thr Thr Arg Leu Cys Asp Ala Met Arg Pro Val Asn Gly Arg						
	405		410		415	
Arg Leu Tyr Lys Asp Phe Val Leu Asn Val Lys Phe Asp Ala Pro Phe						
	420		425		430	
Arg Pro Ala Asp Thr His Asn Glu Val Arg Phe Asp Arg Phe Gly Asp						
	435		440		445	
Gly Ile Gly Arg Tyr Asn Ile Phe Thr Tyr Leu Arg Ala Gly Ser Gly						
	450		455		460	
Arg Tyr Arg Tyr Gln Lys Val Gly Tyr Trp Ala Glu Gly Leu Thr Leu						
465		470		475		480
Asp Thr Ser Leu Ile Pro Trp Ala Ser Pro Ser Ala Gly Pro Leu Pro						
	485		490		495	
Ala Ser Arg Cys Ser Glu Pro Cys Leu Gln Asn Glu Val Lys Ser Val						
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Gln Pro Gly Glu Val Cys Cys Trp Leu Cys Ile Pro Cys Gln Pro Tyr						
	515		520		525	
Glu Tyr Arg Leu Asp Glu Phe Thr Cys Ala Asp Cys Gly Leu Gly Tyr						
	530		535		540	
Trp Pro Asn Ala Ser Leu Thr Gly Cys Phe Glu Leu Pro Gln Glu Tyr						
545		550		555		560
Ile Arg Trp Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys						
	565		570		575	
Leu Gly Ala Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His						
	580		585		590	
Asn Ala Thr Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile						
	595		600		605	

Leu Leu Gly Gly Val Phe Leu Cys Tyr Cys Met Thr Phe Ile Phe Ile
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 Ala Lys Pro Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly
 625 630 635 640
 Thr Ala Phe Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg
 645 650 655
 Ile Ala Arg Ile Phe Gly Gly Ala Arg Glu Gly Ala Gln Arg Pro Arg
 660 665 670
 Phe Ile Ser Pro Ala Ser Gln Val Ala Ile Cys Leu Ala Leu Ile Ser
 675 680 685
 Gly Gln Leu Leu Ile Val Val Ala Trp Leu Val Val Glu Ala Pro Gly
 690 695 700
 Thr Gly Lys Glu Thr Ala Pro Glu Arg Arg Glu Val Val Thr Leu Arg
 705 710 715 720
 Cys Asn His Arg Asp Ala Ser Met Leu Gly Ser Leu Ala Tyr Asn Val
 725 730 735
 Leu Leu Ile Ala Leu Cys Thr Leu Tyr Ala Phe Lys Thr Arg Lys Cys
 740 745 750
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 755 760 765
 Thr Cys Ile Ile Trp Leu Ala Phe Leu Pro Ile Phe Tyr Val Thr Ser
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 835 840 845
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 850 855 860
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 Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr
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 Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly
 965 970 975
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 Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser
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 Leu Glu Ser Ile Met Ala Cys Cys Leu Ser Glu Glu Ala Lys Glu Ala
 1045 1050 1055
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 Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Lys
 1125 1130 1135
 Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala His Ala Gln Leu Val Arg
 1140 1145 1150
 Glu Val Asp Val Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr Val Asp
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Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr Ser Ile 1250 1255 1260		
Met Phe Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val Glu Ser 1265 1270 1275 1280		
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Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Val Asp 1315 1320 1325		
Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala Ala Arg 1330 1335 1340		
Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser Asp Lys 1345 1350 1355 1360		
Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg 1365 1370 1375		
Phe Val Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Lys 1380 1385 1390		
Asp Cys Gly Leu Phe 1395		

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 <211> 905
 <212> PRT
 <213> Chimeric construct ph8SPmGluR4

<400> 48
 Met Val Cys Glu Gly Lys Arg Ser Ala Ser Cys Pro Cys Phe Phe Leu
 1 5 10 15
 Leu Thr Ala Lys Phe Tyr Trp Ile Leu Thr Met Met Gln Arg Thr His
 20 25 30
 Ser Gln Glu Tyr Ala His Ser Ile Arg Ile Asp Gly Asp Ile Thr Leu
 35 40 45
 Gly Gly Leu Phe Pro Val His Gly Arg Gly Ser Glu Gly Lys Pro Cys
 50 55 60
 Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
 65 70 75 80

Phe	Ala	Leu	Asp	Arg	Ile	Asn	Asn	Asp	Pro	Asp	Leu	Leu	Pro	Asn	Ile			
				85					90					95				
Thr	Leu	Gly	Ala	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	His	Ala			
			100					105					110					
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp	Gly			
		115					120					125						
Thr	Glu	Val	Arg	Cys	Gly	Ser	Gly	Gly	Pro	Pro	Ile	Ile	Thr	Lys	Pro			
	130					135					140							
Glu	Arg	Val	Val	Gly	Val	Ile	Gly	Ala	Ser	Gly	Ser	Ser	Val	Ser	Ile			
145					150					155					160			
Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr			
			165						170					175				
Ala	Ser	Thr	Ala	Pro	Asp	Leu	Ser	Asp	Asn	Ser	Arg	Tyr	Asp	Phe	Phe			
			180					185					190					
Ser	Arg	Val	Val	Pro	Ser	Asp	Thr	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp			
	195					200					205							
Ile	Val	Arg	Ala	Leu	Lys	Trp	Asn	Tyr	Val	Ser	Thr	Val	Ala	Ser	Glu			
	210					215					220							
Gly	Ser	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Ile	Gln	Lys	Ser	Arg			
225					230					235					240			
Glu	Asp	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Val	Lys	Ile	Pro	Arg	Glu			
			245						250					255				
Pro	Lys	Ala	Gly	Glu	Phe	Asp	Lys	Ile	Ile	Arg	Arg	Leu	Leu	Glu	Thr			
			260					265					270					
Ser	Asn	Ala	Arg	Ala	Val	Ile	Ile	Phe	Ala	Asn	Glu	Asp	Asp	Ile	Arg			
	275					280						285						
Arg	Val	Leu	Glu	Ala	Ala	Arg	Arg	Ala	Asn	Gln	Thr	Gly	His	Phe	Phe			
	290					295					300							
Trp	Met	Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Leu	His			
305					310					315					320			
Leu	Glu	Glu	Val	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Met			
			325						330					335				
Ser	Val	Arg	Gly	Phe	Asp	Arg	Tyr	Phe	Ser	Ser	Arg	Thr	Leu	Asp	Asn			
			340					345					350					
Asn	Arg	Arg	Asn	Ile	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Asp	Asn	Phe	His			
		355				360					365							
Cys	Lys	Leu	Ser	Arg	His	Ala	Leu	Lys	Lys	Gly	Ser	His	Val	Lys	Lys			
	370					375					380							
Cys	Thr	Asn	Arg	Glu	Arg	Ile	Gly	Gln	Asp	Ser	Ala	Tyr	Glu	Gln	Glu			
385					390					395					400			
Gly	Lys	Val	Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ala	Met	Gly	His	Ala			
			405						410					415				
Leu	His	Ala	Met	His	Arg	Asp	Leu	Cys	Pro	Gly	Arg	Val	Gly	Leu	Cys			
			420					425					430					
Pro	Arg	Met	Asp	Pro	Val	Asp	Gly	Thr	Gln	Leu	Leu	Lys	Tyr	Ile	Arg			
		435					440					445						
Asn	Val	Asn	Phe	Ser	Gly	Ile	Ala	Gly	Asn	Pro	Val	Thr	Phe	Asn	Glu			
	450					455					460							
Asn	Gly	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Tyr	Gln	Tyr	Gln	Leu	Arg			
465					470					475					480			
Asn	Asp	Ser	Ala	Glu	Tyr	Lys	Val	Ile	Gly	Ser	Trp	Thr	Asp	His	Leu			
			485						490					495				
His	Leu	Arg	Ile	Glu	Arg	Met	His	Trp	Pro	Gly	Ser	Gly	Gln	Gln	Leu			
			500					505					510					
Pro	Arg	Ser	Ile	Cys	Ser	Leu	Pro	Cys	Gln	Pro	Gly	Glu	Arg	Lys	Lys			
		515					520					525						
Thr	Val	Lys	Gly	Met	Pro	Cys	Cys	Trp	His	Cys	Glu	Pro	Cys	Thr	Gly			

530		535		540
Tyr Gln Tyr Gln Val Asp Arg Tyr Thr Cys Lys Thr Cys Pro Tyr Asp				
545		550		555
Met Arg Pro Thr Glu Asn Arg Thr Gly Cys Arg Pro Ile Pro Ile Ile				
	565		570	575
Lys Leu Glu Trp Gly Ser Pro Trp Ala Val Leu Pro Leu Phe Leu Ala				
	580		585	590
Val Val Gly Ile Ala Ala Thr Leu Phe Val Val Ile Thr Phe Val Arg				
	595		600	605
Tyr Asn Asp Thr Pro Ile Val Lys Ala Ser Gly Arg Glu Leu Ser Tyr				
	610		615	620
Val Leu Leu Ala Gly Ile Phe Leu Cys Tyr Ala Thr Thr Phe Leu Met				
625		630		635
Ile Ala Glu Pro Asp Leu Gly Thr Cys Ser Leu Arg Arg Ile Phe Leu				
	645		650	655
Gly Leu Gly Met Ser Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn				
	660		665	670
Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys Arg Ser Val Ser Ala Pro				
	675		680	685
Arg Phe Ile Ser Pro Ala Ser Gln Leu Ala Ile Thr Phe Ser Leu Ile				
	690		695	700
Ser Leu Gln Leu Leu Gly Ile Cys Val Trp Phe Val Val Asp Pro Ser				
705		710		715
His Ser Val Val Asp Phe Gln Asp Gln Arg Thr Leu Asp Pro Arg Phe				
	725		730	735
Arg Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Leu Leu				
	740		745	750
Gly Tyr Ser Met Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile Lys				
	755		760	765
Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly Phe				
	770		775	780
Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile Phe				
785		790		795
Phe Gly Thr Ser Gln Ser Ala Asp Lys Leu Tyr Ile Gln Thr Thr Thr				
	805		810	815
Leu Thr Val Ser Val Ser Leu Ser Ala Ser Val Ser Leu Gly Met Leu				
	820		825	830
Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His Pro Glu Gln Asn Val				
	835		840	845
Pro Lys Arg Lys Arg Ser Leu Lys Ala Val Val Thr Ala Ala Thr Met				
	850		855	860
Ser Asn Lys Phe Thr Gln Lys Gly Asn Phe Arg Pro Asn Gly Glu Ala				
865		870		875
Lys Ser Glu Leu Cys Glu Asn Leu Glu Ala Pro Ala Thr Lys Gln Thr				
	885		890	895
Tyr Val Thr Tyr Thr Asn His Ala Ile				
	900		905	

<210> 49

<211> 1416

<212> PRT

<213> Chimeric phmGluR4//CaR*AAA*G_qi5

<400> 49

Met	Val	Cys	Glu	Gly	Lys	Arg	Ser	Ala	Ser	Cys	Pro	Cys	Phe	Phe	Leu
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Leu	Thr	Ala	Lys	Phe	Tyr	Trp	Ile	Leu	Thr	Met	Met	Gln	Arg	Thr	His
			20					25					30		
Ser	Gln	Glu	Tyr	Ala	His	Ser	Ile	Arg	Ile	Asp	Gly	Asp	Ile	Thr	Leu
		35					40					45			
Gly	Gly	Leu	Phe	Pro	Val	His	Gly	Arg	Gly	Ser	Glu	Gly	Lys	Pro	Cys
		50				55					60				
Gly	Glu	Leu	Lys	Lys	Glu	Lys	Gly	Ile	His	Arg	Leu	Glu	Ala	Met	Leu
65					70				75						80
Phe	Ala	Leu	Asp	Arg	Ile	Asn	Asn	Asp	Pro	Asp	Leu	Leu	Pro	Asn	Ile
				85					90					95	
Thr	Leu	Gly	Ala	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	His	Ala
			100					105					110		
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp	Gly
		115					120					125			
Thr	Glu	Val	Arg	Cys	Gly	Ser	Gly	Gly	Pro	Pro	Ile	Ile	Thr	Lys	Pro
		130				135					140				
Glu	Arg	Val	Val	Gly	Val	Ile	Gly	Ala	Ser	Gly	Ser	Ser	Val	Ser	Ile
145					150					155					160
Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr
				165					170					175	
Ala	Ser	Thr	Ala	Pro	Asp	Leu	Ser	Asp	Asn	Ser	Arg	Tyr	Asp	Phe	Phe
			180					185					190		
Ser	Arg	Val	Val	Pro	Ser	Asp	Thr	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp
		195					200					205			
Ile	Val	Arg	Ala	Leu	Lys	Trp	Asn	Tyr	Val	Ser	Thr	Val	Ala	Ser	Glu
		210				215					220				
Gly	Ser	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Ile	Gln	Lys	Ser	Arg
225					230					235					240
Glu	Asp	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Val	Lys	Ile	Pro	Arg	Glu
				245					250					255	
Pro	Lys	Ala	Gly	Glu	Phe	Asp	Lys	Ile	Ile	Arg	Arg	Leu	Leu	Glu	Thr
			260					265					270		
Ser	Asn	Ala	Arg	Ala	Val	Ile	Ile	Phe	Ala	Asn	Glu	Asp	Asp	Ile	Arg
		275					280					285			
Arg	Val	Leu	Glu	Ala	Ala	Arg	Arg	Ala	Asn	Gln	Thr	Gly	His	Phe	Phe
		290				295					300				
Trp	Met	Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Leu	His
305					310					315					320
Leu	Glu	Glu	Val	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Met
				325					330					335	
Ser	Val	Arg	Gly	Phe	Asp	Arg	Tyr	Phe	Ser	Ser	Arg	Thr	Leu	Asp	Asn
			340					345					350		
Asn	Arg	Arg	Asn	Ile	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Asp	Asn	Phe	His
		355					360					365			
Cys	Lys	Leu	Ser	Arg	His	Ala	Leu	Lys	Lys	Gly	Ser	His	Val	Lys	Lys
		370				375					380				
Cys	Thr	Asn	Arg	Glu	Arg	Ile	Gly	Gln	Asp	Ser	Ala	Tyr	Glu	Gln	Glu
385					390					395					400
Gly	Lys	Val	Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ala	Met	Gly	His	Ala
				405					410					415	
Leu	His	Ala	Met	His	Arg	Asp	Leu	Cys	Pro	Gly	Arg	Val	Gly	Leu	Cys
			420					425					430		
Pro	Arg	Met	Asp	Pro	Val	Asp	Gly	Thr	Gln	Leu	Leu	Lys	Tyr	Ile	Arg
		435					440					445			
Asn	Val	Asn	Phe	Ser	Gly	Ile	Ala	Gly	Asn	Pro	Val	Thr	Phe	Asn	Glu
		450				455					460				
Asn	Gly	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Tyr	Gln	Tyr	Gln	Leu	Arg

465		470		475		480
Asn Asp Ser Ala Glu Tyr Lys Val Ile Gly Ser Trp Thr Asp His Leu						
	485		490		495	
His Leu Arg Ile Glu Arg Met His Trp Pro Gly Ser Gly Gln Gln Leu						
	500		505		510	
Pro Arg Ser Ile Cys Ser Leu Pro Cys Gln Pro Gly Glu Arg Lys Lys						
	515		520		525	
Thr Val Lys Gly Met Pro Cys Cys Trp His Cys Glu Pro Cys Thr Gly						
	530		535		540	
Tyr Gln Tyr Gln Val Asp Arg Tyr Thr Cys Lys Thr Cys Pro Tyr Asp						
545	550		555		560	
Met Arg Pro Thr Glu Asn Arg Thr Gly Cys Arg Pro Ile Pro Ile Ile						
	565		570		575	
Lys Leu Glu Trp Gly Ser Pro Trp Ala Val Leu Pro Leu Phe Leu Ala						
	580		585		590	
Val Val Gly Ile Ala Ala Thr Leu Phe Val Val Ile Thr Phe Val Arg						
	595		600		605	
Tyr Asn Asp Thr Pro Ile Val Lys Ala Ser Gly Arg Glu Leu Ser Tyr						
	610		615		620	
Val Leu Leu Ala Gly Ile Phe Leu Cys Tyr Ala Thr Thr Phe Leu Met						
625	630		635		640	
Ile Ala Glu Pro Asp Leu Gly Thr Cys Ser Leu Arg Arg Ile Phe Leu						
	645		650		655	
Gly Leu Gly Met Ser Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn						
	660		665		670	
Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys Arg Ser Val Ser Ala Pro						
	675		680		685	
Arg Phe Ile Ser Pro Ala Ser Gln Leu Ala Ile Thr Phe Ser Leu Ile						
	690		695		700	
Ser Leu Gln Leu Leu Gly Ile Cys Val Trp Phe Val Val Asp Pro Ser						
705	710		715		720	
His Ser Val Val Asp Phe Gln Asp Gln Arg Thr Leu Asp Pro Arg Phe						
	725		730		735	
Arg Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Leu Leu						
	740		745		750	
Gly Tyr Ser Met Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile Lys						
	755		760		765	
Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly Phe						
	770		775		780	
Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile Phe						
785	790		795		800	
Phe Gly Thr Ser Gln Ser Ala Asp Lys Leu Tyr Ile Gln Thr Thr Thr						
	805		810		815	
Leu Thr Val Ser Val Ser Leu Ser Ala Ser Val Ser Leu Gly Met Leu						
	820		825		830	
Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His Pro Glu Gln Asn Thr						
	835		840		845	
Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys Val Ala						
	850		855		860	
Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser Ser						
865	870		875		880	
Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser Ser						
	885		890		895	
Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys Gln						
	900		905		910	
Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu						
	915		920		925	

Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln
 930 935 940
 Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp
 945 950 955 960
 Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser Thr His Gln Asn
 965 970 975
 Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro
 980 985 990
 Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln
 995 1000 1005
 Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val
 1010 1015 1020
 Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser Gln
 1025 1030 1035 1040
 Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val
 1045 1050 1055
 Asn Ser Ala Ala Ala Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu
 1060 1065 1070
 Ser Glu Glu Ala Lys Glu Ala Arg Arg Ile Asn Asp Glu Ile Glu Arg
 1075 1080 1085
 Gln Leu Arg Arg Asp Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu
 1090 1095 1100
 Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met
 1105 1110 1115 1120
 Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe
 1125 1130 1135
 Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile
 1140 1145 1150
 Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys
 1155 1160 1165
 Ala His Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala
 1170 1175 1180
 Phe Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro
 1185 1190 1195 1200
 Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp
 1205 1210 1215
 Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala
 1220 1225 1230
 Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr
 1235 1240 1245
 Gly Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met
 1250 1255 1260
 Val Asp Val Gly Gly Gln Arg Ser Arg Lys Trp Ile His Cys Phe Glu
 1265 1270 1275 1280
 Asn Val Thr Ser Ile Met Phe Leu Val Ser Glu Tyr Asp Gln Val Leu
 1285 1290 1295
 Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe
 1300 1305 1310
 Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu
 1315 1320 1325
 Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His
 1330 1335 1340
 Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln
 1345 1350 1355 1360
 Ala Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp
 1365 1370 1375
 Ser Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu

	1380		1385		1390
Asn	Ile Arg Phe Val Phe Ala	Ala Val Lys Asp Thr	Ile Leu Gln Leu		
	1395	1400	1405		
Asn	Leu Lys Asp Cys Gly Leu Phe				
	1410	1415			

<210> 50

<211> 1411

<212> PRT

<213> Chimeric phmGluR8//CaR*AAA*G q15

<400> 50

Met	Val	Cys	Glu	Gly	Lys	Arg	Ser	Ala	Ser	Cys	Pro	Cys	Phe	Phe	Leu
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Leu	Thr	Ala	Lys	Phe	Tyr	Trp	Ile	Leu	Thr	Met	Met	Gln	Arg	Thr	His
			20					25					30		
Ser	Gln	Glu	Tyr	Ala	His	Ser	Ile	Arg	Val	Asp	Gly	Asp	Ile	Ile	Leu
		35					40					45			
Gly	Gly	Leu	Phe	Pro	Val	His	Ala	Lys	Gly	Glu	Arg	Gly	Val	Pro	Cys
		50				55					60				
Gly	Glu	Leu	Lys	Lys	Glu	Lys	Gly	Ile	His	Arg	Leu	Glu	Ala	Met	Leu
65					70				75					80	
Tyr	Ala	Ile	Asp	Gln	Ile	Asn	Lys	Asp	Pro	Asp	Leu	Leu	Ser	Asn	Ile
				85					90					95	
Thr	Leu	Gly	Val	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala
			100					105					110		
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp	Ala
		115					120					125			
Ser	Asp	Val	Lys	Cys	Ala	Asn	Gly	Asp	Pro	Pro	Ile	Phe	Thr	Lys	Pro
		130				135					140				
Asp	Lys	Ile	Ser	Gly	Val	Ile	Gly	Ala	Ala	Ala	Ser	Ser	Val	Ser	Ile
145					150					155					160
Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr
			165						170					175	
Ala	Ser	Thr	Ala	Pro	Glu	Leu	Ser	Asp	Asn	Thr	Arg	Tyr	Asp	Phe	Phe
			180					185					190		
Ser	Arg	Val	Val	Pro	Pro	Asp	Ser	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp
		195				200					205				
Ile	Val	Thr	Ala	Leu	Gly	Trp	Asn	Tyr	Val	Ser	Thr	Leu	Ala	Ser	Glu
		210			215						220				
Gly	Asn	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Thr	Gln	Ile	Ser	Arg
225					230				235						240
Glu	Ile	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Gln	Lys	Ile	Pro	Arg	Glu
			245					250						255	
Pro	Arg	Pro	Gly	Glu	Phe	Glu	Lys	Ile	Ile	Lys	Arg	Leu	Leu	Glu	Thr
			260					265					270		
Pro	Asn	Ala	Arg	Ala	Val	Ile	Met	Phe	Ala	Asn	Glu	Asp	Asp	Ile	Arg
		275				280					285				
Arg	Ile	Ala	Ala	Lys	Lys	Leu	Asn	Gln	Ser	Gly	His	Phe	Leu	Trp	Ile
		290				295					300				
Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Tyr	Gln	Gln	Glu
305					310				315						320
Glu	Ile	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Ala	Ser	Ile
			325					330					335		
Asp	Gly	Phe	Asp	Arg	Tyr	Phe	Arg	Ser	Arg	Thr	Leu	Ala	Asn	Asn	Arg
			340					345					350		

Arg	Asn	Val	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Glu	Asn	Phe	Gly	Cys	Lys	
		355					360				365					
Leu	Gly	Ser	His	Gly	Lys	Arg	Asn	Ser	His	Ile	Lys	Lys	Cys	Thr	Gly	
	370					375					380					
Leu	Glu	Arg	Ile	Ala	Arg	Asp	Ser	Ser	Tyr	Glu	Gln	Glu	Gly	Lys	Val	
385					390					395					400	
Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ser	Met	Ala	Tyr	Ala	Leu	His	Asn	
				405					410					415		
Met	His	Lys	Asp	Leu	Cys	Pro	Gly	Tyr	Ile	Gly	Leu	Cys	Pro	Arg	Met	
			420					425					430			
Ser	Thr	Ile	Asp	Gly	Lys	Glu	Leu	Leu	Gly	Tyr	Ile	Arg	Ala	Val	Asn	
		435					440					445				
Phe	Asn	Gly	Ser	Ala	Gly	Thr	Pro	Val	Thr	Phe	Asn	Glu	Asn	Gly	Asp	
	450					455					460					
Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Phe	Gln	Tyr	Gln	Ile	Thr	Asn	Lys	Ser	
465					470					475					480	
Thr	Glu	Tyr	Lys	Val	Ile	Gly	His	Trp	Thr	Asn	Gln	Leu	His	Leu	Lys	
				485					490					495		
Val	Glu	Asp	Met	Gln	Trp	Ala	His	Arg	Glu	His	Thr	His	Pro	Ala	Ser	
			500					505					510			
Val	Cys	Ser	Leu	Pro	Cys	Lys	Pro	Gly	Glu	Arg	Lys	Lys	Thr	Val	Lys	
		515					520					525				
Gly	Val	Pro	Cys	Cys	Trp	His	Cys	Glu	Arg	Cys	Glu	Gly	Tyr	Asn	Tyr	
	530					535					540					
Gln	Val	Asp	Glu	Leu	Ser	Cys	Glu	Leu	Cys	Pro	Leu	Asp	Gln	Arg	Pro	
545					550					555					560	
Asn	Met	Asn	Arg	Thr	Gly	Cys	Gln	Leu	Ile	Pro	Ile	Ile	Lys	Leu	Glu	
				565					570					575		
Trp	His	Ser	Pro	Trp	Ala	Val	Val	Pro	Val	Phe	Val	Ala	Ile	Leu	Gly	
			580					585					590			
Ile	Ile	Ala	Thr	Thr	Phe	Val	Ile	Val	Thr	Phe	Val	Arg	Tyr	Asn	Asp	
		595					600					605				
Thr	Pro	Ile	Val	Arg	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	Val	Leu	Leu	
	610					615					620					
Thr	Gly	Ile	Phe	Leu	Cys	Ile	Thr	Phe	Leu	Met	Ile	Ala	Ala	Pro	Asp	
625					630					635					640	
Thr	Ile	Ile	Cys	Ser	Phe	Arg	Arg	Val	Phe	Leu	Gly	Leu	Gly	Met	Cys	
			645						650					655		
Phe	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Ile	His	Arg	Ile	
			660					665					670			
Phe	Glu	Gln	Gly	Lys	Lys	Ser	Val	Thr	Ala	Pro	Lys	Phe	Ile	Ser	Pro	
		675					680					685				
Ala	Ser	Gln	Leu	Val	Ile	Thr	Phe	Ser	Leu	Ile	Ser	Val	Gln	Leu	Leu	
	690					695					700					
Gly	Val	Phe	Val	Trp	Phe	Val	Val	Asp	Pro	Pro	His	Ile	Ile	Ile	Asp	
705					710					715					720	
Tyr	Gly	Glu	Gln	Arg	Thr	Leu	Asp	Pro	Glu	Lys	Arg	Val	Leu	Lys	Cys	
			725						730					735		
Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	Ser	Leu	Gly	Tyr	Ser	Ile	Leu	
			740					745					750			
Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala	Ile	Lys	Thr	Arg	Gly	Val	Pro	
		755					760					765				
Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	Gly	Phe	Thr	Met	Tyr	Thr	Thr	
	770					775					780					
Cys	Ile	Ile	Trp	Leu	Ala	Phe	Ile	Pro	Ile	Phe	Phe	Gly	Thr	Ala	Gln	
785					790					795					800	
Ser	Ala	Glu	Lys	Met	Tyr	Ile	Gln	Thr	Thr	Thr	Leu	Thr	Val	Ser	Met	

				805					810					815			
Ser	Leu	Ser	Ala	Ser	Val	Ser	Leu	Gly	Met	Leu	Tyr	Met	Pro	Lys	Val		
			820					825					830				
Tyr	Ile	Ile	Ile	Phe	His	Pro	Glu	Gln	Asn	Thr	Ile	Glu	Glu	Val	Arg		
		835						840				845					
Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val	Ala	Ala	Arg	Ala	Thr	Leu		
	850					855					860						
Arg	Arg	Ser	Asn	Val	Ser	Arg	Lys	Arg	Ser	Ser	Ser	Leu	Gly	Gly	Ser		
865				870					875						880		
Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser	Ser	Lys	Ser	Asn	Ser	Glu		
			885						890				895				
Asp	Pro	Phe	Pro	Gln	Pro	Glu	Arg	Gln	Lys	Gln	Gln	Gln	Pro	Leu	Ala		
			900					905					910				
Leu	Thr	Gln	Gln	Glu	Gln	Gln	Gln	Gln	Pro	Leu	Thr	Leu	Pro	Gln	Gln		
		915						920				925					
Gln	Arg	Ser	Gln	Gln	Gln	Pro	Arg	Cys	Lys	Gln	Lys	Val	Ile	Phe	Gly		
	930					935				940							
Ser	Gly	Thr	Val	Thr	Phe	Ser	Leu	Ser	Phe	Asp	Glu	Pro	Gln	Lys	Asn		
945				950					955						960		
Ala	Met	Ala	His	Gly	Asn	Ser	Thr	His	Gln	Asn	Ser	Leu	Glu	Ala	Gln		
			965					970					975				
Lys	Ser	Ser	Asp	Thr	Leu	Thr	Arg	His	Gln	Pro	Leu	Leu	Pro	Leu	Gln		
			980					985					990				
Cys	Gly	Glu	Thr	Asp	Leu	Asp	Leu	Thr	Val	Gln	Glu	Thr	Gly	Leu	Gln		
		995					1000				1005						
Gly	Pro	Val	Gly	Gly	Asp	Gln	Arg	Pro	Glu	Val	Glu	Asp	Pro	Glu	Glu		
	1010					1015					1020						
Leu	Ser	Pro	Ala	Leu	Val	Val	Ser	Ser	Ser	Gln	Ser	Phe	Val	Ile	Ser		
1025				1030					1035						1040		
Gly	Gly	Gly	Ser	Thr	Val	Thr	Glu	Asn	Val	Val	Asn	Ser	Ala	Ala	Ala		
			1045					1050					1055				
Met	Thr	Leu	Glu	Ser	Ile	Met	Ala	Cys	Cys	Leu	Ser	Glu	Glu	Ala	Lys		
			1060					1065					1070				
Glu	Ala	Arg	Arg	Ile	Asn	Asp	Glu	Ile	Glu	Arg	Gln	Leu	Arg	Arg	Asp		
		1075					1080				1085						
Lys	Arg	Asp	Ala	Arg	Arg	Glu	Leu	Lys	Leu	Leu	Leu	Leu	Gly	Thr	Gly		
	1090					1095					1100						
Glu	Ser	Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln	Met	Arg	Ile	Ile	His	Gly		
1105				1110					1115						1120		
Ser	Gly	Tyr	Ser	Asp	Glu	Asp	Lys	Arg	Gly	Phe	Thr	Lys	Leu	Val	Tyr		
			1125						1130				1135				
Gln	Asn	Ile	Phe	Thr	Ala	Met	Gln	Ala	Met	Ile	Arg	Ala	Met	Asp	Thr		
			1140					1145				1150					
Leu	Lys	Ile	Pro	Tyr	Lys	Tyr	Glu	His	Asn	Lys	Ala	His	Ala	Gln	Leu		
		1155					1160					1165					
Val	Arg	Glu	Val	Asp	Val	Glu	Lys	Val	Ser	Ala	Phe	Glu	Asn	Pro	Tyr		
		1170				1175					1180						
Val	Asp	Ala	Ile	Lys	Ser	Leu	Trp	Asn	Asp	Pro	Gly	Ile	Gln	Glu	Cys		
1185				1190					1195						1200		
Tyr	Asp	Arg	Arg	Arg	Glu	Tyr	Gln	Leu	Ser	Asp	Ser	Thr	Lys	Tyr	Tyr		
			1205						1210				1215				
Leu	Asn	Asp	Leu	Asp	Arg	Val	Ala	Asp	Pro	Ala	Tyr	Leu	Pro	Thr	Gln		
			1220					1225					1230				
Gln	Asp	Val	Leu	Arg	Val	Arg	Val	Pro	Thr	Thr	Gly	Ile	Ile	Glu	Tyr		
		1235				1240					1245						
Pro	Phe	Asp	Leu	Gln	Ser	Val	Ile	Phe	Arg	Met	Val	Asp	Val	Gly	Gly		
	1250					1255					1260						

Gln	Arg	Ser	Arg	Lys	Trp	Ile	His	Cys	Phe	Glu	Asn	Val	Thr	Ser	Ile
1265					1270					1275					1280
Met	Phe	Leu	Val	Ser	Glu	Tyr	Asp	Gln	Val	Leu	Val	Glu	Ser	Asp	Asn
				1285					1290					1295	
Glu	Asn	Arg	Met	Glu	Glu	Ser	Lys	Ala	Leu	Phe	Arg	Thr	Ile	Ile	Thr
			1300					1305					1310		
Tyr	Pro	Trp	Phe	Gln	Asn	Ser	Ser	Val	Ile	Leu	Phe	Leu	Asn	Lys	Lys
		1315				1320						1325			
Asp	Leu	Leu	Glu	Glu	Lys	Ile	Met	Tyr	Ser	His	Leu	Val	Asp	Tyr	Phe
	1330					1335					1340				
Pro	Glu	Tyr	Asp	Gly	Pro	Gln	Arg	Asp	Ala	Gln	Ala	Ala	Arg	Glu	Phe
1345					1350				1355						1360
Ile	Leu	Lys	Met	Phe	Val	Asp	Leu	Asn	Pro	Asp	Ser	Asp	Lys	Ile	Ile
			1365					1370					1375		
Tyr	Ser	His	Phe	Thr	Cys	Ala	Thr	Asp	Thr	Glu	Asn	Ile	Arg	Phe	Val
		1380				1385						1390			
Phe	Ala	Ala	Val	Lys	Asp	Thr	Ile	Leu	Gln	Leu	Asn	Leu	Lys	Asp	Cys
	1395					1400						1405			
Gly	Leu	Phe													
	1410														

1265 1270 1275 1280
 1285 1290 1295
 1300 1305 1310
 1315 1320 1325
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 1380 1385 1390
 1395 1400 1405
 1410